

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 06:48:07 : Search time 3020 Seconds

(without alignments)
10417.263 Million cell updates/sec

Title: US-10-010-568-1

Perfect score: 1081

Sequence: 1 catattgccaaactgactc.....ccttgaatattcattac 1081

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:*

1: gb_ba:*

2: gb_hlg:*

3: gb_in:*

4: gb_om:*

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6: gb_pat:*

7: gb_ph:*

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14: gb_vl:*

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19: em_mu:*

20: em_om:*

21: em_or:*

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32: em_hlg_other:*

33: em_hlg_mus:*

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39: em_hlg_hum:*

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41: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1081	100.0	1081	6	AX458238
2	1081	100.0	1414	6	AB065877
3	1081	100.0	9905	6	AX379470
4	1081	100.0	67645	9	AL356486
5	1081	100.0	156555	9	AC026756
6	1079.4	99.9	1729	6	AX191332
7	1046	96.8	1092	6	AF370886
8	1014	93.8	1014	6	AX148186
9	1014	93.8	1014	6	AX379468
10	1014	93.8	1014	6	AX384211
11	1014	93.8	1014	9	AB083598
12	1014	93.8	1014	9	AF411109
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19	242	22.4	657	6	AX244775
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22	158.6	14.7	3204	10	RN022830
23	153.8	14.2	12630	2	MM024536
24	153.8	14.2	288763	2	AC124692
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ALIGNMENTS

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AX458238

LOCUS AX458238 1081 bp DNA linear PAT 08-JUL-2002

DEFINITION Sequence 1 from Patent WO024614.

ACCESSION AX458238

VERSION AX458238.1 GI:21724972

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Ramanathan, C., Feder, J., Nelson, T., Cacace, A., Barber, L. and Rysek, R.P.

A novel human g-protein coupled receptor, hgrbm23, expressed

TITLE

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NMF"
BASE COUNT      376 a      337 c      260 g      441 t
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Best Local Similarity 100.0%; Pred. No. 9,3e-271;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATATTGCCAACTGAAGTCTCTGTTTCTTGGCAAGTGAAGAGCAACATGAATG 60
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NMF"
BASE COUNT      376 a      337 c      260 g      441 t
ORIGIN
Query Match      100.0%; Score 1081; DB 9; Length 1414;
Best Local Similarity 100.0%; Pred. No. 9,3e-271;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATATTGCCAACTGAAGTCTCTGTTTCTTGGCAAGTGAAGAGCAACATGAATG 60
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QY 61 AGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTATGACGCTCTTTGGAA 120
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QY 121 ATTGCACTGATGAAACATGCCACTCAAGATGCACTACCTCCGTTATTTATGACATTA 180
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RESULT 3
AX379470
LOCUS
DEFINITION Sequence 3 from Patent WO0187980.
ACCESSION AX379470
VERSION AX379470.1 GI:19575227
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1. Wei, M.H., Zhao, Q.C., Cravchik, A.C., di Francesco, V.C. and
Beasley, E.M.
Isolated human g-protein coupled receptors, nucleic acid molecules
encoding human gpcr proteins, and uses thereof
Patent: WO 0187980-A 3 22-NOV-2001;
Aplera Corporation Robert A. Millman Assistant Secretary (US)
LOCATION/Qualifiers
1. 9905
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Best Local Similarity 100.0%; Pred. No. 9,7e-271;
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Db 4064 C 4064

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VERSION AC026756
KEYWORDS AC026756.15 GI:13112251
SOURCE HTG.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15655)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federapfel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.U., Nguyen,M.,
Oefner,P., Palm,C.U., Ramirez,D., Southwick,A.M., Wilhelm,J.,
Yu,S. and Davis,R.W.

JOURNAL
Unpublished

REFERENCE		2 (bases 1 to 156555)
AUTHORS		Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Fedorisiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Mao,J., Marathe,R., Morehouse,A.U., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmly,J., Yu,S. and Davis,R.W. Direct Submission Submitted (23-MAR-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
TITLE		3 (bases 1 to 156555).
JOURNAL		
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AUTHORS		On Feb 23, 2001 this sequence version replaced gi:12745089.
TITLE		----- Genome Center
JOURNAL		Center: Stanford DNA Sequencing and Technology Development Center
COMMENT		Center code: SNSTDC Web site: http://sequence-www.stanford.edu/group/human/ Contact: hum-info@sequence.stanford.edu ----- Project Information Center project name: 870 Center clone name: RP11-286P8
FEATURES		----- Summary This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. Location/Qualifiers source 1..156555 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="13" /clone="RP11-286P8" /clone_id="RPC1 human BAC library 11"
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Db 1321 C 1321

RESULT 7

AF370886 1092 bp mRNA linear PRI 11-JUL-2002

LOCUS Homo sapiens G protein-coupled receptor GPR99 (GPR99) mRNA, complete cds.

ACCESSION AF370886 GI:21728283

VERSION AF370886.1

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1092)

AUTHORS Wittenberger, T., Heilebrand, S., Munk, A., Kreienkamp, H.J., Schaller, H.C. and Hampe, W.

TITLE GPR99, a new G protein-coupled receptor belonging to a new subgroup of nucleotide receptors

JOURNAL BMC Genomics 3 (1), 17 (2002)

PUBMED 12098360

REFERENCE 2 (bases 1 to 1092)

AUTHORS Hampe, W.

TITLE Direct Submission

JOURNAL Submitted (17-APR-2001) Developmental Neurobiology, Zentrum fuer Molekulare Neurobiologie, Martinistr. Hamburg 20246, Germany

FEATURES

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Qy 156 TACCTCCCTGTTATTTATGCAATTAATCTTCTGAGGAAATTCAGAGCAATGAGTAA 215

Db 121 TACCTCCCTGTTATTTATGCAATTAATCTTCTGAGGAAATTCAGAGCAATGAGTAA 180

Qy 216 ATATGCACTTACATTTTCAAAATGAGACCTTGAAGAGCAACCATTAATGCTGAAC 275

Db 181 ATATGCACTTACATTTTCAAAATGAGACCTTGAAGAGCAACCATTAATGCTGAAC 240

Qy 276 CTGACCTGACAGATCTGCTGATCTGACAGAGCTCCCTGCTGATCACTATGCT 335

Db 241 CTGACCTGACAGATCTGCTGATCTGACAGAGCTCCCTGCTGATCACTATGCT 300

Qy 336 AGTGGGAAACTGATCTTTGAGATTCATGATGATTAATCCGCTTACAGCTTCAT 395

Db 301 AGTGGGAAACTGATCTTTGAGATTCATGATGATTAATCCGCTTACAGCTTCAT 360

Qy 396 TTCAACCTGTATGAGAGATCTCTTCTGACCTGTTTCAAGCAATCTTCCGTAATG 455

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Qy 456 ATCAATTCACCAATGAGCTTTTCCATTCACAAACCTGATGACATGATGAGCTGT 515

Db 421 ATCAATTCACCAATGAGCTTTTCCATTCACAAACCTGATGAGCTGT 480

Qy 516 GCTGTGTGTGATCATTTTCACTGTGAGCTGATTCGATGACCTTCTTGAATCAATCA 575

Db 481 GCTGTGTGTGATCATTTTCACTGTGAGCTGATTCGATGACCTTCTTGAATCAATCA 540

Qy 576 ACCAAGAGGACCAAGATCAGCTGCTGTGACCTTCACAGTGTGAGTAATCAATACT 635

Db 541 ACCAAGAGGACCAAGATCAGCTGCTGTGACCTTCACAGTGTGAGTAATCAATACT 600

Qy 636 ATTAAGTGTACAACTGATTTTGAATCTGCAATCTTCTGCTCCCTTGTGATAGT 695

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Db 781 TTACCTTCAATCTTGAAGGTCATTCGATGCAATCTGCTGCTTCAATCAATGATGT 840

Qy 876 TCCATGAGATCAATCAATGAGCTTCAATGCTTTTCAAGCAATGAGCTGCTGAAC 935

Db 841 TCCATGAGATCAATCAATGAGCTTCAATGCTTTTCAAGCAATGAGCTGCTGAAC 900

Qy 936 ACCTTGTAACTGTAATATGCTGTGCTGAGGCAACTTTTCAAGAGCTGTCTGC 995

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BASE COUNT	258 a	263 c	189 g	304 t	ORIGIN
Query Match	93.8%	Score 1014	DB 6	Length 1014	
Best Local Similarity	100.0%	Pred. No. 2.7e-253			
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QY	54	ATGAAATGAGCACTAGACGCTATTTAGCAAAATGCTTCTGATTTTCCCGATTTATGACAGCTGCT	113		
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DB	121	GCGATATCTTCTCGTGGGATTTTCCAGGCAATGAGTATGATATCCACTTACATTTTC	180		
QY	234	AAATATGAGCTTTGGAAGAGCAGCAACATCATTTATGCTGAACCTGGCTGCAAGATCTG	293		
DB	181	AAATATGAGCTTTGGAAGAGCAGCAACATCATTTATGCTGAACCTGGCTGCAAGATCTG	240		
QY	294	CTGTATCTGACAGAGCTCCCTCCGTGATTCCTATATGCAATGCAATGCGAGGAAATCTGATC	353		
DB	241	CTGTATCTGACAGAGCTCCCTCCGTGATTCCTATATGCAATGCAATGCGAGGAAATCTGATC	300		
QY	354	TTTGGAGATTTGATGTGTAAGTTATTCGCGCTTCAAGCTTCAATTTCAACCTGTATGAGAC	413		
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QY	414	ATCTCTTCTCACTGCTGTTTACAGATCTTCCGCTATCTGTGATCATTTCAACCAATGAGC	473		
DB	361	ATCTCTTCTCACTGCTGTTTACAGATCTTCCGCTATCTGTGATCATTTCAACCAATGAGC	420		
QY	474	TGCTTTTCCATTCACAAAATCTGATGACATTTGAGCTGTGCTGTGTGTGATCATTT	533		
DB	421	TGCTTTTCCATTCACAAAATCTGATGACATTTGAGCTGTGCTGTGTGTGATCATTT	480		
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DB	481	TCACGTGATGCTGATTCGATTCGATGACCTTCTTGTATCATATCAACCAAGAGCAACGAG	540		
QY	594	TCAGCTGTCTGACCTTCAACGATTCGATGACATCATTTAATGAGTGTGATCAACCTG	653		
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QY	1014	GTAAGCGGAGACCTTGGAGCAAGAAAATGATTACTCAAAACAACCTTGA	1067		

TITLE Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
 Direct Submission
 Submitted (17-AUG-2001) Department of Pharmacology, University of
 Toronto, 8 Raddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A6, Canada
 FEATURES Location/Qualifiers

SOURCE

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 /db_xref="taxon:9606"
 /chromosome="13"

gene

<1..>1014
 /gene="GPR80"

mRNA

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CDS

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 SLVAVIPWFLITSRTNRNSACLDLSSDEINIKMNLILATFPLPIVITLY
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 NNP"

BASE COUNT 258 a 263 c 189 g 304 t
 ORIGIN

Query Match 93.8%; Score 1014; DB 9; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 2.7e-253; Indels 0; Gaps 0;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ATGAATAGCCACTAGACTATTATAGCAAAATGCTTGATTTCCCGATTATGACCTGCT 113
 DB 1 ATGAATAGCCACTAGACTATTATAGCAAAATGCTTGATTTCCCGATTATGACCTGCT 60
 QY 114 TTGGAAATGGCACTGATGAAACATCCCACTCAAGATGCACTCTCCCTGTTATTTAT 173
 DB 61 TTGGAAATGGCACTGATGAAACATCCCACTCAAGATGCACTCTCCCTGTTATTTAT 120
 QY 174 GGCATTATCTTCCTGAGGATTTCCAGCAATGCAAGATGATTCACCTTACATTTTC 233
 DB 121 GGCATTATCTTCCTGAGGATTTCCAGCAATGCAAGATGATTCACCTTACATTTTC 180
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 DB 181 AAAATGAGCCTTGAAGAGACGACCATTTATGCTGAACCTGGCCGACAGATCTG 240
 QY 294 CTGTATCTGACAGCCTTCCCTCTGATTCATGCACTATGCAAGTGGGAAAATGATC 353
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 QY 354 TTGGAGATTTCAATGATGATTTATCGCTTCAGCTTCATTTCAACCTGATAGCAGC 413
 DB 301 TTGGAGATTTCAATGATGATTTATCGCTTCAGCTTCATTTCAACCTGATAGCAGC 360
 QY 414 ATCCCTCTTCCCACTGTTTCAAGATCTTGCTACTAGTGTGATCATCCCAATGAGC 473
 DB 361 ATCCCTCTTCCCACTGTTTCAAGATCTTGCTACTAGTGTGATCATCCCAATGAGC 420
 QY 474 TGGTTTTCATTCACAAATCTGATGATGATTTAGCTGTGCTGTGTGATCATTT 533
 DB 421 TGGTTTTCATTCACAAATCTGATGATGATTTAGCTGTGCTGTGTGATCATTT 480
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QY 654 ATTTTGAATGCACTACTATTTCTGCTCCCTTGGTGAATGACATTTGCTATACAGC 713
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 QY 1014 GTAAAGCGGAACTTTGAGCAAGCAAAAGAAATTAATGTTACTCAACCAACCTTGA 1067
 DB 961 GTAAAGCGGAACTTTGAGCAAGCAAAAGAAATTAATGTTACTCAACCAACCTTGA 1014

RESULT 13

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 LOCUS AX305130
 DEFINITION Sequence 10 from Patent WO0187937.
 ACCESSION AX305130
 VERSION AX305130.1 GI:17644765
 KEYWORDS

SOURCE

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Paterson, C., Lu, D.A., Thornton, M., Lu, Y., Tribouley, C.M.,
 Graul, R., Khan, F.A., Gandhi, A.R., Walla, N.K., Nguyen, D.B., Yue, H.,
 Hafalia, A., Elliott, V.S., Lal, P., Reddy, R., Kallick, D.A., Tang, T.Y.
 and Au-Young, J.
 G-protein coupled receptors
 Patent: WO 0187937-A 10 22-NOV-2001;
 Incyte Genomics, Inc. (US)

TITLE

JOURNAL

FEATURES

SOURCE

1. 1014
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /note="Incyte ID No: 6575963CB1"

BASE COUNT

ORIGIN

Query Match 93.7%; Score 1012.4; DB 6; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 6.9e-253;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 54 ATGAATAGCCACTAGACTATTATAGCAAAATGCTTGATTTCCCGATTATGACCTGCT 113
 DB 1 ATGAATAGCCACTAGACTATTATAGCAAAATGCTTGATTTCCCGATTATGACCTGCT 60
 QY 114 TTGGAAATGGCACTGATGAAACATCCCACTCAAGATGCACTCTCCCTGTTATTTAT 173
 DB 61 TTGGAAATGGCACTGATGAAACATCCCACTCAAGATGCACTCTCCCTGTTATTTAT 120
 QY 174 GGCATTATCTTCCTGAGGATTTCCAGCAATGCAAGATGATTCACCTTACATTTTC 233
 DB 121 GGCATTATCTTCCTGAGGATTTCCAGCAATGCAAGATGATTCACCTTACATTTTC 180

DR P-PSDB; AA014027.
 XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterized by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies
 XX
 XX Claim 23; Fig 3; 64bp; English.
 PS
 CC The present specifically claimed human genomic DNA sequence (located on
 CC chromosome 13) encodes a purinergic-related G-protein coupled receptor
 CC (GPCR) of the invention. GPCRs constitute a major class of proteins
 CC responsible for signal transduction within a cell. Upon binding of a
 CC ligand to the extracellular portion of a GPCR, a signal is transduced
 CC resulting in a biological or physiological change within the cell. The
 CC GPCR proteins can be divided into five families, family 1 contains the
 CC purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are
 CC characterized by their selective responsiveness towards ATP and its
 CC analogues, some also respond to UTP. The invention comprises a human
 CC G-protein coupled receptor protein and encoding nucleic acids. The GPCR
 CC protein and nucleic acids of the invention are useful in the treatment of
 CC a disease or condition mediated by a human protease. The GPCR protein of
 CC the invention is useful for the development/identification of
 CC therapeutic proteins; assays designed to quantitatively determine levels
 CC of the protein in biological fluids; identifying compounds which modulate
 CC the activity of the GPCR, or the interaction of the GPCR and a molecule
 CC with which it normally interacts; and treating a disorder characterized
 CC by an absence of, or inappropriate expression of the GPCR protein. The
 CC GPCR nucleic acids of the invention are useful in: diagnostic assays to
 CC identify changes in the GPCR nucleic acid that lead to pathology;
 CC controlling GPCR expression; and in gene therapy to treat patients with
 CC aberrant GPCR gene expression. The GPCR nucleic acids can also be used in
 CC the production of transgenic animals.
 XX
 XX Sequence 9905 BP; 2656 A; 2218 C; 2061 G; 2970 T; 0 other;

Query Match 100.0%; Score 1081; DB 24; Length 9905;
 Best Local Similarity 100.0%; Pred. No. 1.9e-306;
 Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 121 ATTGCACTGATGAAGAAATCCCACTCAAGATGACACTCCCTGTTATTTATGAGCATTA 180
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 QY 181 TCTTCTCGTGGGATTTCCAGGCAATGCAATGATGATTCATCTACATTTTCAAAAAGA 240
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 QY 421 TCCCTCACTGTTTCAAGACTTCCGCTACTGATGATCATTCACCCATGAGCGCTTTT 480
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Db 8736 CCATTGCAAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 8795
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 QY 661 CTGCAACTACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 8916 CTGCAACTACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8975
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 QY 1081 C 1081
 Db 9336 C 9336

RESULT 3
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 AC AAS08362;
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 DT 26-SEP-2001 (first entry)
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 XX
 KW Human; G-protein coupled receptor; GPCR; 39404; immunogen; antibody;
 KW Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;
 KW Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
 KW systemic lupus erythematosus; actinic keratosis; myocarditis;
 KW Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasm;
 KW inflammations; teratoma; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 FT /-tag= a
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 XX
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 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI
 XX Schlegel R, Endege WO, Monahan JE;
 XX
 DR MPI, 2001-662795/76.
 XX

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1, Page 4453-4454; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;

Query Match 99.9%; Score 1079.4; DB 23; Length 1729;
 Best Local Similarity 99.9%; Pred. No. 2.3e-306;
 Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 61 AGCCACTAAGCTATTAGCAAAATGCTTCTGATTTCCCGATTATGACGCTGCTTTGAA 120
 DB 301 AGCCACTAAGCTATTAGCAAAATGCTTCTGATTTCCCGATTATGACGCTGCTTTGAA 360
 QY 121 ATTGCACTGATGAAGAACTCCCACTCAAGATGCACTACTCCCTGTTATTTATGACATTA 180
 DB 361 ATTGCACTGATGAAGAACTCCCACTCAAGATGCACTACTCCCTGTTATTTATGACATTA 420
 QY 181 TCTTCTCGTGGGATTTCCAGGAATGCAATGATGATACCTATTCATTTTCAAAATGA 240
 DB 421 TCTTCTCGTGGGATTTCCAGGAATGCAATGATGATACCTATTCATTTTCAAAATGA 480
 QY 241 GACCTTGAAGACACACATCATTTATGCTGAACCTGAGCTGACAGATCTGCTGATC 300
 DB 481 GACCTTGAAGACACACATCATTTATGCTGAACCTGAGCTGACAGATCTGCTGATC 540
 QY 301 TGACCAAGCTCCCTCTCTGATTCATCTATGACCAAGTGGCGAAAATGATCTTTGAG 360
 DB 541 TGACCAAGCTCCCTCTCTGATTCATCTATGACCAAGTGGCGAAAATGATCTTTGAG 600
 QY 361 ATTGATGATGAAGTTATCCGCTTCAAGCTTCAATTTCAACCTGATATGAGAGATCTCT 420
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QY 481 CCATTACAAAACCTGATGTGAGTTGATGACCTGCTGTGTGATCATTTCACTG 540
 DB 721 CCATTACAAAACCTGATGTGAGTTGATGACCTGCTGTGTGATCATTTCACTG 780
 QY 541 TAGCTGATTCGATGACCTGCTGATGACCTGATGACCTGATGACCTGATGACCT 600
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 DB 841 GTCTGACCTGACCTGATGACCTGATGACCTGATGACCTGATGACCTGATGACCT 900
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 DB 901 CTGCAACTACTTCTGCTCCCTGCTGATGATGATGATGATGATGATGATGATGAT 960
 QY 721 ACACTGACCTGACCTGATGACCTGATGACCTGATGACCTGATGACCTGATGACCT 780
 DB 961 ACACTGACCTGACCTGATGACCTGATGACCTGATGACCTGATGACCTGATGACCT 1020
 QY 781 CCATTGCTGATGACCTGATGACCTGATGACCTGATGACCTGATGACCTGATGACCT 840
 DB 1021 CCATTGCTGATGACCTGATGACCTGATGACCTGATGACCTGATGACCTGATGACCT 1080
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 DB 1201 TGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
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 QY 1081 C 1081
 DB 1321 C 1321

RESULT 5
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 ID ABV25767 standard; cDNA; 1729 BP.
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 AC ABV25767;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25758.
 XX
 KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US051171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX

prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1: Page 6451; 11750bp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a patient;

(I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 1729 BP, 461 A; 401 C; 302 G; 548 T; 17 other;

PS Claim 1; Page 6451; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (AB700010-AB962213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC XX
 S0 Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
 Query Match 99.9%; Score 1079.4; DB 23; Length 1729;
 Best Local Similarity 99.9%; Pred. No. 2.3e-306;
 Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0

SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;

Query Match	99.9%	Score 1079.4	DB 23	Length 1729
Best Local Similarity	99.9%	Pred. No. 23e-306		
Matches 1080, Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	1	CATATGCGAAACTGAAACTCTGTGTTTCTTGCAAGATGAAAGAGACAAACCTGATG	60
Db	241	CATATGCGAAACTGAACTCTGTGTTTCTTGCAAGATGAAAGAGACAAACCTGATG	300
QY	61	AGCGCATAGACTATTAGCAAAATGCTTCTGATTTCCCGATTATGACAGCTTTGGAA	120
Db	301	AGCGCATAGACTATTAGCAAAATGCTTCTGATTTCCCGATTATGACAGCTTTGGAA	360
QY	121	ATTGCACTGATGATAAAACATGCCCTGAAGTGCATCACTCCCTGTATTATGCGATT	180
Db	361	ATTGCACTGATGATAAAACATGCCCTGAAGTGCATCACTCCCTGTATTATGCGATT	420
QY	181	TCTTCTCGTGGGATTTCCAGGCAATGCAGTAGTAGTATCCATTTATTTCAAAATGA	240
Db	421	TCTTCTCGTGGGATTTCCAGGCAATGCAGTAGTAGTATCCATTTATTTCAAAATGA	480
QY	241	GACCTTGGAAAGCAGCAGCATCATATATGCTGAACCTGGCTGACAGATCTGCTGATC	300
Db	481	GACCTTGGAAAGCAGCAGCATCATATATGCTGAACCTGGCTGACAGATCTGCTGATC	540
QY	301	TGACCAAGCTCCCTTCCCTGATTCACTATATGCGAGTGGCGAAAACCTGATCTTTGGAG	360
Db	541	TGACCAAGCTCCCTTCCCTGATTCACTATATGCGAGTGGCGAAAACCTGATCTTTGGAG	600
QY	361	ATTTCATGATGATGATTTATCCGCTTCAGCTTCCATTTCAACCTGATAGAGATCTCTG	420
Db	601	ATTTCATGATGATGATTTATCCGCTTCAGCTTCCATTTCAACCTGATAGAGATCTCTG	660
QY	421	TCTCTACCTGTTTCAGCATCTTCCGCTACTGTGTGATCAATTCACCCAAATGAGCTGCTTT	480
Db	661	TCTCTACCTGTTTCAGCATCTTCCGCTACTGTGTGATCAATTCACCCAAATGAGCTGCTTT	720
QY	481	CCATTCACAAAACCTGAGATGTGAGTTGTAACCTGCTGTGGTGTGATCACTTCACTGG	540
Db	721	CCATTCACAAAACCTGAGATGTGAGTTGTAACCTGCTGTGGTGTGATCACTTCACTGG	780
QY	541	TAGCTGTATTCCGATGACCTTCTTGATCATCATCAACCAAGGACCAACATCAAGCTT	600
Db	781	TAGCTGTATTCCGATGACCTTCTTGATCATCATCAACCAAGGACCAACATCAAGCTT	840
QY	601	GTCCTGACCTCAACCAAGTTGCGATGAACCTCAATATTAAGTGTGCAACCTGATTTGA	660
Db	841	GTCCTGACCTCAACCAAGTTGCGATGAACCTCAATATTAAGTGTGCAACCTGATTTGA	900
QY	661	CTGCAACTACTTTCTGCTCCCTCTGGTGTGATGTGACATTTGCTATACCAAGATTATCC	720

Db	901	CTGGACACTACTTTCGCTCCCTCCCTTGGTATGACACTTTGGTATACACGATTATCC	960
Qy	721	AACACTTCACCCATGAGCTGCAAACTGACAGCTGCCTTAAGACAAAGACGAGCTAA	780
Db	961	AACACTTCACCCATGAGCTGCAAACTGACAGCTGCCTTAAGACAAAGACGAGCTAA	1020
Qy	781	CCATTCTGCTACTCTGCTGCAATTTTACGTATGTTTTTAACTCCCTTCATATCTTAAAGGCTCA	840
Db	1021	CCATTCTGCTACTCTGCTGCAATTTTACGTATGTTTTTAACTCCCTTCATATCTTAAAGGCTCA	1080
Qy	841	TTCCGATGGAATCTCGCTGCTTCATACAGTGTCTTCATTTGGAATTCAGATCCATGAAG	900
Db	1081	TTCCGATGGAATCTCGCTGCTTCATACAGTGTCTTCATTTGGAATTCAGATCCATGAAG	1140
Qy	901	CTTACATCGTTTCTAGACCAATTAGCTGCTCTGAAACACCTTTGGTAACTGTACTATATG	960
Db	1141	CTTACATCGTTTCTAGACCAATTAGCTGCTCTGAAACACCTTTGGTAACTGTACTATATG	1200
Qy	961	TGCTGTGACGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAGTAAGCG	1020
Db	1201	TGCTGTGACGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAGTAAGCG	1260
Qy	1021	GGAACCTTGAGCAGCAAGAAATTAAGTACTCAAAACACCTTGAATATTTCACTTAA	1080
Db	1261	GGAACCTTGAGCAGCAAGAAATTAAGTACTCAAAACACCTTGAATATTTCACTTAA	1320
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Db	1321	C 1321	
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ID	ABV30024	standard; cDNA; 1729 BP.	
XX	ABV30024;		
AC	16-SEP-2002	(first entry)	
DT			
XX			
DE	Human prostate expression marker	cdna 30015.	
XX			
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;		
KW	pharmacogenomic marker; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200160860-A2.		
XX			
FD	23-AUG-2001.		
XX			
PF	20-FEB-2001; 2001WO-US05171.		
XX			
PR	17-FEB-2000; 2000US-183319P.		
PR	16-MAR-2000; 2000US-189862P.		
PR	25-MAY-2000; 2000US-207454P.		
PR	09-JUN-2000; 2000US-211314P.		
PR	18-JUL-2000; 2000US-219007P.		
PR	13-DEC-2000; 2000US-255281P.		
XX			
PA	(MILL-) MILLENNium PREDICTIVE MEDICINE INC.		
XX			
PI	Schlegel R, Endege WO, Monahan JE;		
XX			
XX	WPI; 2001-662795/76.		
DR			
PT	Novel isolated nucleic acid molecule associated with cancerous state of		
PT	prostate cells and correlating with presence of prostate cancer, useful		
PT	for detecting presence of prostate cancer, stage of prostate cancer		
XX			
PS	Claim 1; Page 6487-6488; 11750DP; English.		
XX			
XX	The invention relates to an isolated nucleic acid molecule (I) comprising		
CC	a nucleotide sequence given in Tables 1-9 (aunononabunuc2217) of		

XX	RESULT 7
XX	ABV30024
XX	ABV30024 standard; cDNA, 1729 BP.
XX	
AC	ABV30024;
XX	
DT	16-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker cDNA 30015.
XX	
KM	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX	pharmacogenomic marker; gene; ss.
OS	
XX	Homo sapiens.
PN	
XX	WO200160860-A2.
PD	
XX	23-AUG-2001.
PF	
XX	20-FEB-2001; 2001WO-US05171.
PR	
XX	17-FEB-2000; 2000US-183319P.
PR	16-MAR-2000; 2000US-189862P.
XX	25-MAY-2000; 2000US-207454P.
PR	09-JUN-2000; 2000US-211314P.
PR	18-JUL-2000; 2000US-219007P.
XX	13-DEC-2000; 2000US-255281P.
PA	
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI	
XX	Schlegel R, Endege WO, Monahan JE;
DR	
XX	WPI; 2001-662795/76.
PT	
XX	Novel isolated nucleic acid molecule associated with cancerous state of
PT	prostate cells and correlating with presence of prostate cancer, useful
XX	for detecting presence of prostate cancer, stage of prostate cancer
XX	
XX	Claim 1; Page 6487-6488; 11750P; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	a nucleotide sequence given in Tables 1-9 (bnu001n.bnu2211) of

CC sequence is that of the p2Y11 encoding cDNA.

XX Sequence 1288 BP; 347 A; 318 C; 241 G; 382 T; 0 other;

SQ Query Match 96.7%; Score 1045; DB 24; Length 1288;

Best Local Similarity 100.0%; Pred. No. 2,6e-296;

Matches 1045; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 97 CCGATTATGACGCTGCTTTGGAATGCACTGATGAAACATCCCACTCAAGATGACT 156
Db 61 CCGATTATGACGCTGCTTTGGAATGCACTGATGAAACATCCCACTCAAGATGACT 120
Oy 157 ACCCTCCGTTATTTAAGGCACTTATCTTCTGCGGGAATTTCCAGGCAATGAGTAGTA 216
Db 121 ACCCTCCGTTATTTAAGGCACTTATCTTCTGCGGGAATTTCCAGGCAATGAGTAGTA 180
Oy 217 TATCCACTTACATTTTCAAAATGAGACCTTGGAAAGAGACCATCATTTAGCTGAACC 276
Db 181 TATCCACTTACATTTTCAAAATGAGACCTTGGAAAGAGACCATCATTTAGCTGAACC 240
Oy 277 TGGCTGACAGATCTGCTGATCTGACAGCTCCCTTCTGATTCATCTACTATGCGCA 336
Db 241 TGGCTGACAGATCTGCTGATCTGACAGCTCCCTTCTGATTCATCTACTATGCGCA 300
Oy 337 GTGGCCAAAAGCTGGATCTTTGGAATTTGATGTGAATTTATCCGCTTCAGCTTCAAT 396
Db 301 GTGGCCAAAAGCTGGATCTTTGGAATTTGATGTGAATTTATCCGCTTCAGCTTCAAT 360
Oy 397 TCAACCTGATAGAGATCTCTCTCAACCTGTTTCAAGATCTTCCGCTACTGTGTGA 456
Db 361 TCAACCTGATAGAGATCTCTCTCAACCTGTTTCAAGATCTTCCGCTACTGTGTGA 420
Oy 457 TCAATTCACCAATGAGCTGCTTTTCCATTCACAAATCTGATGAGATTTAGCTGTG 516
Db 421 TCAATTCACCAATGAGCTGCTTTTCCATTCACAAATCTGATGAGATTTAGCTGTG 480
Oy 517 CTGTGTGTGATGATTCATCTGCTGATCTGTGATCCGATGACCTTCTTGAATCAATCA 576
Db 481 CTGTGTGTGATGATTCATCTGCTGATCTGTGATCCGATGACCTTCTTGAATCAATCA 540
Oy 577 CCAAGGAGACCAACATGATGAGCTGTCTGACCTTCAACGTTTGGATGAATCAATCTA 636
Db 541 CCAAGGAGACCAACATGATGAGCTGTCTGACCTTCAACGTTTGGATGAATCAATCTA 600
Oy 637 TTAAGTGTACACCTGATTTTGAAGTGAAGTCTTCTGCTCCCTTGGTGTATGTA 696
Db 601 TTAAGTGTACACCTGATTTTGAAGTGAAGTCTTCTGCTCCCTTGGTGTATGTA 660
Oy 697 CACTTTGTAATCCAGATATTCACACTGTAACCCATGAGTGAAGTGAAGTGAAGTGC 756
Db 661 CACTTTGTAATCCAGATATTCACACTGTAACCCATGAGTGAAGTGAAGTGAAGTGC 720
Oy 757 TTAAGGAGAAAGAGAGAGCTTACCACTTCTGCTACTCTTGAATTTTACGATGTTTT 816
Db 721 TTAAGGAGAAAGAGAGAGCTTACCACTTCTGCTACTCTTGAATTTTACGATGTTTT 780
Oy 817 TACCTTCATATCTTGAAGGATCATCGATGCAATTCGCCGCTTTCATCAATGTTT 876
Db 781 TACCTTCATATCTTGAAGGATCATCGATGCAATTCGCCGCTTTCATCAATGTTT 840
Oy 877 CCAATGAGATCAGATCAGATGAGCTTACATCTTTCTAGACATTTAGCTGCTGTAACA 936
Db 841 CCAATGAGATCAGATCAGATGAGCTTACATCTTTCTAGACATTTAGCTGCTGTAACA 900
Oy 937 CTTTGTGTAACCTGTTACTATATGTGTGTGTCAGGCAACCTTTCAGCAGGCTGTGCT 996
Db 901 CTTTGTGTAACCTGTTACTATATGTGTGTGTCAGGCAACCTTTCAGCAGGCTGTGCT 960
Oy 997 CAACAGTAGATGCAAAAGTAAGCGGGAACCTTGAAGCAAGCAAAATAATTAATTA 1056

```

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Db 961 ACAAGTAGATGCAAAAGTAAGCGGGAACCTTGAAGCAAGCAAAATAATTAATTA 1020
Oy 1057 ACAACCTTGAATATTTTCAATTAC 1081
Db 1021 ACAACCTTGAATATTTTCAATTAC 1045

RESULT 9
AAS07948
ID AAS07948 standard; cDNA; 1014 BP.
XX
AC AAS07948;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human cDNA encoding G-protein coupled receptor, hRUP21.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP21; agonist;
KW Inverse agonist; lung cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1014
FT /tag= a
FT /product= "hRUP21"

WO200136471-A2.
XX
PD 25-MAY-2001.
XX
XX 16-NOV-2000; 2000WO-US31509.
XX
XX 17-NOV-1999; 99US-0166088.
XX 17-NOV-1999; 99US-0166099.
XX 17-NOV-1999; 99US-0166369.
XX 23-DEC-1999; 99US-0171900.
XX 23-DEC-1999; 99US-0171901.
XX 23-DEC-1999; 99US-0171902.
XX 11-FEB-2000; 2000US-0181749.
XX 14-MAR-2000; 2000US-0189258.
XX 14-MAR-2000; 2000US-0189259.
XX 10-APR-2000; 2000US-0195899.
XX 10-APR-2000; 2000US-0195899.
XX 10-APR-2000; 2000US-0196078.
XX 28-APR-2000; 2000US-0200419.
XX 12-MAY-2000; 2000US-0203630.
XX 12-JUN-2000; 2000US-0210741.
XX 12-JUN-2000; 2000US-0210982.
XX 21-AUG-2000; 2000US-0226760.
XX 26-SEP-2000; 2000US-0235418.
XX 26-SEP-2000; 2000US-0235418.
XX 20-OCT-2000; 2000US-0242332.
XX 20-OCT-2000; 2000US-0242343.
XX
XX (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Lowitz KP,
XX
XX WPI; 2001-355616/37.
XX
XX P-PSDB; AAV04375.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents -
PS
PS Claim 55; Page 113-114; 159pp; English.
XX
XX The sequence encodes a human G-protein coupled receptor (GPCR),
XX hRUP21. The endogenous and non-endogenous, constitutively activated
XX versions of human G-protein coupled receptors (GPCR), are useful for
XX direct identification of candidate compounds as receptor agonists.

```


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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 06:48:56 : Search time 2177 Seconds

(without alignments)
8041.948 Million cell updates/sec

Title: US-10-010-568-1

Perfect score: 1081

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin:*
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8: em_hcc:*
9: gb_est1:*
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11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	23.8	744	14	BM723768 UI-E-BO1-BM723768
2	126.6	11.7	623	14	BQ038875 pgnlc.pk0
3	115.6	10.7	641	14	BQ396255 NISC_ng19
4	114.6	10.6	638	9	AL675845 AL675845
5	109.4	10.1	877	12	BG402029 602466748
6	108.8	10.1	663	13	BM426517 pgfzn.pk0

Result No.	Score	Query Match	Length	DB ID	Description
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9	103	9.5	609	9	AL588350
10	102	9.4	520	9	AL663305
11	100.4	9.3	2542	11	AK017378
12	100.4	9.3	3001	11	AK005013
13	100	9.3	422	10	BB847918
14	99.6	9.2	801	13	BQ924078
15	98.4	9.1	606	17	AZ953874
16	97.2	9.0	851	13	BI833118
17	96	8.9	639	10	BB660768
18	95.8	8.9	408	13	BI401676
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31	91.6	8.5	678	10	BB314834
32	89.8	8.3	589	14	BQ396804
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35	87.6	8.1	752	13	BM008116
36	87.6	8.1	801	13	BI837965
37	87.6	8.1	870	9	AL545172
38	87.6	8.1	885	9	AL546894
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41	87.2	8.1	529	9	AA177828
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ALIGNMENTS

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DEFINITION
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BM723768
VERSION
BM723768.1 GI:19045099
SOURCE
EST.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 744)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: ms0atres@iuc.wieg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. W. Bento Soares, University of Iowa

KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 641)
NIH-XGC http://image.llnl.gov/image/html/xenopuslib_info.shtml.
TITLE National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLML1977 row: N column: 13
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insert size 2.1 kb. Constructed by Invitrogen. Note: This
is a Xenopus Gene Collection (XGC) library."
BASE COUNT 132 a 184 c 153 g 172 t
ORIGIN
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Best Local Similarity 51.8%; Pred. No. 4,5e-22;
Matches 262; Conservative 0; Mismatches 244; Indels 0; Gaps 0;
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DB 185 ACATTCGGCCCTGATCACTTCTGTTCCGATCAAGCCCTGGAAGCCTCCACACCT 244
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DB 245 ACATTTCAACTGGGCATTTCCGACATGATGACATCTCCCTCCCGCTGCTGCT 304
QY 325 ACTATGATGCGAGGCGGAAACTGGATCTTTGGAATTTCAATGTAATTTATCCGCT 384
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QY 445 GCTACTGTGATCATTCACCAATGAGCTGCTTTTTCATTCACAAATCGATGTCAG 504
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QY 505 TTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
DB 485 GGATATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 544
QY 565 TGATCATCATCAACCAAGAGCAACAGATGAGCCCTGCTGCACTCCACAGTTGGAGT 624
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QY 625 AACTCAATCTATTAAGTGATCAAC 650
DB 605 TATTTGACACATTTGCTGTACAC 630
RESULT 4
LOCUS AL675845
DEFINITION AL675845 XGC-gastrula Silurana tropicalis cDNA clone Tga505ln19 5',
mRNA sequence.
ACCESSION AL675845
VERSION AL675845.1 GI:19532219
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 638)
Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: Tga505ln19.p1csp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
source
1..638
Location/Qualifiers
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Tga505ln19"
/clone_11b="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from 5' of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
BASE COUNT 134 a 180 c 144 g 179 t 1 others
ORIGIN
Query Match 10.6%; Score 114.6; DB 9; Length 638;
Best Local Similarity 51.6%; Pred. No. 8,8e-22;
Matches 261; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 145 TCAAGATGACATCACTCCCTGTTATTTATGAGCATTAATCTTCCCTGGGATTTCCAGGCA 204
DB 121 TCAAGTACGTCCTCTCCCGGTGTCGACGAGATCGTTCGCGGGCGGATGATCTGA 180
QY 205 ATGAGTAGATGATATCACTTACATTTTCAAAATGAGACCTTGAAGAGAGACCATCA 264
DB 181 ACATTCGGCCCTGATCACTTCTGTTCCGATCAAGCCCTGGAAGCCTCCACACCT 240
QY 265 TTATGCTGAACCTGGCTGACAGATCTGCTATCTGACAGCCCTCCCTTCCTGATTC 324
DB 241 ACATTTCAACTGGGCATTTCCGACATGATGACATCTCCCTCCCGCTGCTGCT 300
QY 325 ACTATGATGCGAGGCGGAAACTGGATCTTTGGAATTTCAATGTAATTTATCCGCT 384
DB 301 ATTACTACTCGGAGGGGCAACTGGCCGTCGCGCTGCTGCTGCTGCTGCTGCT 360
QY 385 TCAGTTCCATTTCAACCTGATAGAGAGATCTCTTCCACCTGTTTCAAGATTTCC 444
DB 361 TCCCTTTTCAACCAAGATGATGATGATCTCTCTTCTGCTGTCATCAAGATCAC 420
QY 445 GCTACTGTGATCATTCACCAATGAGCTGCTTTTTCATTCACAAATCGATGTCAG 504

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/note="Genoscope sequence ID : COAA020AG11C1-end : T7"
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone_id="Normalized Liver Library"
/bex="Male and Female"
/tissue_type="liver"
/lab_host="E. coli EMDH10B"

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Db 488 GATTCGTGAACCCCATGAGGCAAGGCAAGAGGCAACATCGCCGTTGGCTTCCTT 547
 Qy 515 TGCTGTGGGTGATCATTTCACTGGTAGCTGC 548
 Db 548 GGCATCTGCTCTCTGATTTTCTGTGATCACCATC 581

RESULT 15

AZ953874

606 bp DNA 1linear GSS 27-APR-2001

LOCUS

2M0219117F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

DEFINITION

Clone UUGC2M0219117 F, DNA sequence.

ACCESSION

AZ953874

VERSION

AZ953874.1 GI:13825101

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: 1 column: 17
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 606.
Location/Qualifiers

FEATURES

1..606
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0219117"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

100 a 203 c 145 g 158 t

ORIGIN

Query Match

9.1%; Score 98.4; DB 17; Length 606;

Best Local Similarity 57.2%; Pred. No. 4e-17;
 Matches 199; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
 Qy 270 CTGAACCTGGCTGCAAGATCTGCTGATCTGACAGCCTCCCTTCTGATTCATAC 329
 Db 160 CTGAACCTGGCTGCAAGATCTGCTGATCTGACAGCCTCCCTTCTGATTCATAC 219
 Qy 330 TATGCGAGTGGGAAACCTGATCTTGGAGATTTGATGTGATGATTTATCGCTTACG 389
 Db 220 TATGCGAGTGGGAAACCTGATCTTGGAGATTTGATGTGATGATTTATCGCTTACG 279
 Qy 390 TTCCATTTCAACCTGATAGACAGATCTCTTCCACCTGTTTCAAGATCTTCCGTAC 449
 Db 280 TTCTATGCCATCTATATGACAGATCTCTTCCACCTGTTTCAAGATCTTCCGTAC 339
 Qy 450 TGTGTGATCATTCACCCATGAGCTGCTTTCATTCACAAAATGAGTGCAGTT--- 506
 Db 340 CTGGGATCTGCGACACCCCTGCTTCTGCGACAAAGTGGAGTGGCTGCTTGG 399
 Qy 507 GTAGCTGTGCTGT 566
 Db 400 GTAGT 459
 Qy 567 ATCAATCAACCAAGACAGACCAAGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGT 614
 Db 460 GCTGCCATGATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 507

Search completed: January 30, 2003, 11:05:45
 Job time : 2204 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 30, 2003, 03:10:53 ; Search time 59 Seconds

(without alignments)
5618.942 Million cell updates/sec

Title: US-10-010-568-1

Perfect score: 1081
Sequence: 1 catattgccaaactgaactc.....ccttgaataattcattac 1081

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/bckfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	129	11.9	1996	2	US-08-559-524A-1 Sequence 1, Appl1
2	129	11.9	1996	3	US-08-749-707-1 Sequence 1, Appl1
3	103.2	9.5	1842	1	US-08-442-134A-1 Sequence 1, Appl1
4	103.2	9.5	1842	1	US-08-444-581B-1 Sequence 1, Appl1
5	103.2	9.5	1842	1	US-08-446-088A-1 Sequence 1, Appl1
6	100	9.3	984	3	US-08-513-974B-41 Sequence 1, Appl1
7	100	9.3	1020	3	US-08-513-974B-370 Sequence 370, App
8	97.8	9.0	1475	1	US-08-097-938-1 Sequence 1, Appl1
9	97.8	9.0	1475	1	US-08-476-000-1 Sequence 1, Appl1
10	97.8	9.0	1475	1	US-08-472-840-1 Sequence 1, Appl1
11	97.8	9.0	1475	2	US-08-476-976-1 Sequence 1, Appl1
12	97.8	9.0	1475	2	US-08-474-410-1 Sequence 1, Appl1
13	97.8	9.0	1475	4	US-08-486-673B-1 Sequence 1, Appl1
14	97.8	9.0	2732	1	US-08-476-000-60 Sequence 1, Appl1
15	97.8	9.0	2732	1	US-08-472-840-60 Sequence 60, Appl1
16	97.8	9.0	2732	2	US-08-476-976-60 Sequence 60, Appl1
17	97.8	9.0	2732	3	US-08-474-410-60 Sequence 60, Appl1
18	97.8	9.0	2732	4	US-08-486-673B-60 Sequence 60, Appl1
19	95.8	8.9	984	3	US-08-513-974B-57 Sequence 57, Appl1
20	95.8	8.9	1023	3	US-08-513-974B-379 Sequence 379, App
21	94.2	8.7	984	3	US-08-459-046-1 Sequence 1, Appl1
22	92.8	8.6	1102	2	US-08-742-440A-5 Sequence 5, Appl1
23	92.8	8.6	1224	2	US-08-742-440A-4 Sequence 4, Appl1
24	90.8	8.4	1901	1	US-08-153-848-43 Sequence 43, Appl1
25	90.8	8.4	1901	3	US-09-299-843A-43 Sequence 43, Appl1
26	90.8	8.4	1901	4	US-09-088-337B-43 Sequence 43, Appl1
27	90.8	8.4	1901	5	PCT-US93-11153-43 Sequence 43, Appl1

28	90.8	8.4	2453	5	PCT-US95-07180-1 Sequence 1, Appl1
29	87.2	8.1	1224	2	US-08-742-440A-1 Sequence 1, Appl1
30	84	7.8	1317	1	US-08-153-848-45 Sequence 45, Appl1
31	84	7.8	1317	3	US-09-299-843A-45 Sequence 45, Appl1
32	84	7.8	1317	5	US-09-088-337B-45 Sequence 45, Appl1
33	84	7.8	1317	5	PCT-US93-11153-45 Sequence 45, Appl1
34	84	7.8	1664	4	US-09-582-224A-5 Sequence 5, Appl1
35	84	7.8	1679	4	US-09-517-605-14 Sequence 14, Appl1
36	84	7.8	1737	1	US-08-202-056-4 Sequence 4, Appl1
37	84	7.8	1737	1	US-08-076-093A-3 Sequence 3, Appl1
38	84	7.8	1737	2	US-08-701-265-3 Sequence 3, Appl1
39	84	7.8	1737	2	US-08-284-586-3 Sequence 3, Appl1
40	84	7.8	1737	2	US-08-805-478-3 Sequence 3, Appl1
41	84	7.8	1737	2	US-08-802-627A-3 Sequence 3, Appl1
42	84	7.8	1737	2	US-08-801-238-3 Sequence 3, Appl1
43	84	7.8	1737	2	US-08-801-228-3 Sequence 3, Appl1
44	84	7.8	1737	3	US-09-104-296-3 Sequence 3, Appl1
45	84	7.8	1737	5	PCT-US94-06380-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-559-524A-1
Sequence 1, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL FORINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 625..1626
US-08-559-524A-1

Query Match 11.9%; Score 129; DB 2; Length 1996;
Best Local Similarity 50.1%; Pred. No. 1,482-29;
Matches 380; Conservative 0; Mismatches 370; Indels 9; Gaps 2;
QY 108 GCGCTTTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGT 167

APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-41

Query Match 9.3%; Score 100; DB 3; Length 984;
Best Local Similarity 57.5%; Pred. No. 7.2e-21;
Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;
QY 270 CTGAACCTGGCGCTGACAGATCTGCTATCTGACACGCTCCCTTCTCTATTCACATAC 329
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DB 256 TAGCCGAGGAGGACCACTGCGCCCTTGAGAACCTCGCGCTTGTGAGCTTCTC 315
QY 390 TTCCATTTCAACCTGTATAGAGAGATCTCTCTCACTTCTTTCAGATCTTCCGCTAC 449
DB 316 TTCTATGCCAATCAATAGGAGATCTGTCTTCTCACTTCAAGCTTCAAGGCTAC 375
QY 450 TGTGTATCAATCAACCAATAGAGCTGCTTTTCATTCACAAACTCGATGTGCAAGT--- 506
DB 376 CTGGGCAATTCGCCACCCCTGCTCTCCGCAAGCTGAGGTGCGCGCTGCTGG 435
QY 507 GTAGCCTGTGCTGTGTGTGATGATTTCACTGTGAGTGTGTCATTCGATACCTTCTTG 566
DB 436 GTAGTGTGTGAGAGTGTGTGCTGTGTGACAGCCAGTGTGCTGCGCCAGCGAGTCTTT 495
QY 567 ATCAATCAACCAAGAGCAAGATCAAGATCAAGCTGTCTGACCTGACC 614

DB 496 GCTGCCAGGCAATCCAGCCGCAACCGCACTGTGTCTACGACCTGAGC 543
RESULT 7
US-08-513-974B-370
Sequence 370, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400

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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 232..1416
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 232
US-08-476-000-1

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Query Match          9.0%; Score 97.8; DB 1; Length 1475;
Best Local Similarity 52.6%; Pred. No. 4.3e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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QY 144 CTGAAGATGACCTACCTCCCTGTTATTATGAGATATCTCTCCGAGATTTCAGGC 203
DB 442 CTGACACGAGCTCTTCTTCGGTCGTACATTATGTTGTGATGTTGGCCAGT 501
QY 204 AATGACATGATATCCACTTACATTTTCAAAATGAGACCTTGAAGAGACAGACATC 263
DB 502 AATGACATGAGCCCTCGATCTTCTTTCGACAGAGAAAGAACCCCGCGGAT 561
QY 264 ATTATGCTGAACCTGGCTGCAAGATCTGCTGATCTGACAGCCTCCCTTCTGATT 323
DB 562 TACATGGCCAACTGGCCCTGGCCGACCTCTCTGTCATCTGTTCCCTCGAAGATC 621
QY 324 CACTACTATGCAAGTGGGCAAAATGAGATCTTGAAGATTTCACTGTGATATCCGC 383
DB 622 TCTTACCACTTACATGGAACAACCTGGCTCTAGCGGAGGACCTCTGCAAGGTCTCAT 681
QY 384 TTGAGCTTCCATTCAACCTGTATAGCAGATCTCTTCTTCACTGTTTCAAGATCTTC 443
DB 682 GGCCTTTTCTATGTAACATGATATGCTCCATCTCTTATGACCTGCTCAGCGTCAG 741
QY 444 CGTACTGTGTGATCATTCACCCAAATGAGCTCTTTTCATTTCACAAATCGATGTGA 503
DB 742 AGTACTGGGTGATGTGAACCCCATGGAGACCCAGAGAAAGCAACATCGCGCT 801
QY 504 GTTGTAGCTGTGCTGTGTGTGATCATTTTCACTGTGATGCTGTG 548
DB 802 GGCCTTCTTGGCAATCTGGCTCTGATTTTCTGTGATCAATC 846

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RESULT 10
US-08-472-840-1
Sequence 1, Application US/08472840
Patent No. 5763575
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

```

```

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,840
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 232..1416
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 232
US-08-472-840-1

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Query Match          9.0%; Score 97.8; DB 1; Length 1475;
Best Local Similarity 52.6%; Pred. No. 4.3e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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QY 144 CTGAAGATGACCTACCTCCCTGTTATTATGAGATATCTCTCCGAGATTTCAGGC 203
DB 442 CTGACACGAGCTCTTCTTCGGTCGTACATTATGTTGTGATGTTGGCCAGT 501
QY 204 AATGACATGATATCCACTTACATTTTCAAAATGAGACCTTGAAGAGACAGACATC 263
DB 502 AATGACATGAGCCCTCGATCTTCTTTCGACAGAGAAAGAACCCCGCGGAT 561
QY 264 ATTATGCTGAACCTGGCTGCAAGATCTGCTGATCTGACAGCCTCCCTTCTGATT 323
DB 562 TACATGGCCAACTGGCCCTGGCCGACCTCTCTGTCATCTGTTCCCTCGAAGATC 621
QY 324 CACTACTATGCAAGTGGGCAAAATGAGATCTTGAAGATTTCACTGTGATATCCGC 383
DB 622 TCTTACCACTTACATGGAACAACCTGGCTCTAGCGGAGGACCTCTGCAAGGTCTCAT 681
QY 384 TTGAGCTTCCATTCAACCTGTATAGCAGATCTCTTCTTCACTGTTTCAAGATCTTC 443
DB 682 GGCCTTTTCTATGTAACATGATATGCTCCATCTCTTATGACCTGCTCAGCGTCAG 741
QY 444 CGTACTGTGTGATCATTCACCCAAATGAGCTCTTTTCATTTCACAAATCGATGTGA 503
DB 742 AGTACTGGGTGATGTGAACCCCATGGAGACCCAGAGAAAGCAACATCGCGCT 801
QY 504 GTTGTAGCTGTGCTGTGTGTGATCATTTTCACTGTGATGCTGTG 548
DB 802 GGCCTTCTTGGCAATCTGGCTCTGATTTTCTGTGATCAATC 846

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RESULT 11
US-08-476-976-1

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Db 562 TACATGCGCACTGGAGCTTGGCCGACCTCTCTGTCTCATCTGCTTCCCCCTGAAATATC 621
Qy 324 CACTACTATGCAAGTGGCGAAACCTGATCTTGGAGATTTCATGTGTATGTTATTCGCC 383
Db 622 TCTTACCACTTACATGCAACATGGGCTTACGGGAGGCCCTGTGCAAGGTCTCATTT 681
Qy 384 TTGACCTTTCATTTCACCTGTATATGACAGCATCTCTTCTCACTGTTTCCAGATCTTC 443
Db 682 GGCCTTTTCTATGTGTAACATGATATGCTCATCTCTTATGATGACCTCCCTACGCGTACG 741
Qy 444 CGCTACTGTGTATCATTTCAACCAATGAGCTGCTTTTCCATTGACAAACTGATGTCA 503
Db 742 AGGTACTGGGTATCTGTGAACCCCATGGAGCAACCCAGAAAGGCAACATGCGCGTT 801
Qy 504 GTTGTAGCTGT 548
Db 802 GCGCTCTCTTGTGCAATCTGGCTCTGCTGATTTTCTGTGTATCCATTC 846

RESULT 13

US-08-486-673B-1
Sequence 1, Application US/08486673B
Patent No. 6297026
GENERAL INFORMATION:
APPLICANT: Sundelin, Johan
TITLE OF INVENTION: Nucleic Acids Encoding the C140 Receptor
FILE REFERENCE: 44481-5006-08-US
CURRENT APPLICATION NUMBER: US/08/486,673B
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/097,938
PRIOR FILING DATE: 1993-07-26
PRIOR APPLICATION NUMBER: PCT/US94/08536
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1475
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (232)..(1416)
OTHER INFORMATION: C140 receptor, genomic DNA and deduced protein
OTHER INFORMATION: sequences
US-08-486-673B-1

Query Match 9.0%; Score 97.8; DB 4; Length 1475;
Best Local Similarity 52.6%; Pred. No. 4.3e-20;

Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 144 CTCAAGATGCACTACCTCCCTGTTATTTATGACATTATCTCTGCGGATTTCCAGGC 203
Db 442 CTGACCAAGGCTTTCTTCGCGGTCTTACATTTATGTTGTTGTAATGTTGTTGCCAGT 501
Qy 204 AATGCAATGATATTCATCTTAATTTCAAAATGAGACCTTGGAGAAGCAGACCATTC 263
Db 502 AATGCGATGGCCCTCTGATCTTCCTTTCCGAGAGAAAGAAACACCCGCCCTGATTT 561
Qy 264 AATATGCTGAACCTGGCTGCAAGATTTGCTGATCTGACCAAGCTTCCCTCTGATTT 323
Db 562 TACATGCGCAACCTGGCTTGGCGACCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 621
Qy 324 CACTACTATGCAAGTGGCGAAACCTGATCTTGGAGATTTCATGTGTATGTTATTCGCC 383
Db 622 TCTTACCACTTACATGCAACATGGGCTTACGGGAGGCCCTGTGCAAGGTCTCATTT 681
Qy 384 TTGACCTTTCATTTCACCTGTATATGACAGCATCTCTTCTCACTGTTTCCAGATCTTC 443
Db 682 GGCCTTTTCTATGTGTAACATGATATGCTCATCTCTTATGATGACCTCCCTACGCGTACG 741
Qy 444 CGCTACTGTGTATCATTTCAACCAATGAGCTGCTTTTCCATTGACAAACTGATGTGCA 503

Db 742 AGGTACTGGGTATCTGTGAACCCCATGGAGCAACCCAGAAAGGCAACATGCGCGTT 801
Qy 504 GTTGTAGCTGT 548
Db 802 GCGCTCTCTTGTGCAATCTGGCTCTGCTGATTTTCTGTGTATCCATTC 846

RESULT 14

US-08-476-000-60
Sequence 60, Application US/08476000
Patent No. 5716789
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,000
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 2732 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1269
US-08-476-000-60

Query Match 9.0%; Score 97.8; DB 1; Length 2732;
Best Local Similarity 52.6%; Pred. No. 6e-20;

Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 144 CTCAAGATGCACTACCTCCCTGTTATTTATGACATTATCTCTGCGGATTTCCAGGC 203
Db 225 CTGACCAAGGCTTTCTTCGCGGTCTTACATTTATGTTGTTGTAATGTTGTTGCCAGT 354
Qy 204 AATGCAATGATATTCATCTTAATTTCAAAATGAGACCTTGGAGAAGCAGACCATTC 263
Db 355 AATGCGATGGCCCTCTGATCTTCCTTTCCGAGAGAAAGAAACACCCGCCCTGATTT 414
Qy 264 AATATGCTGAACCTGGCTGCAAGATTTGCTGATCTGACCAAGCTTCCCTCTGATTT 323
Db 415 TACATGCGCAACCTGGCTTGGCGACCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 474
Qy 324 CACTACTATGCAAGTGGCGAAACCTGATCTTGGAGATTTCATGTGTATGTTATTCGCC 383

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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 04:05:55 (Search time 69 Seconds
(without alignments)
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Perfect score: 1081
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgm2_6/ptodata/1/pubpna/ECT_NEW_PUB.seq:*
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- 10: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgm2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgm2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgm2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgm2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	93.8	1014	US-09-943-798-3	Sequence 3, Appl1
2	831	76.9	831	US-09-943-798-1	Sequence 1, Appl1
3	779.4	72.1	1313	US-09-728-422-1	Sequence 1, Appl1
4	515	47.6	526	US-09-812-102-40	Sequence 40, Appl1
5	93.6	8.7	993	US-09-826-791-1	Sequence 1, Appl1
6	93.6	8.7	1041	US-09-826-478-1	Sequence 1, Appl1
7	93.6	8.7	1041	US-09-826-791-5	Sequence 5, Appl1
8	93.6	8.7	1041	US-09-866-230-6	Sequence 6, Appl1
9	93.6	8.7	1430	US-09-828-478-3	Sequence 3, Appl1
10	93.6	8.7	1700	US-09-728-952-26	Sequence 26, Appl1
11	90.8	8.4	1020	US-09-788-133-1	Sequence 1, Appl1
12	84	7.8	1670	US-09-880-107-1143	Sequence 2143, Ap
13	84	7.8	1737	US-09-104-063-3	Sequence 3, Appl1
14	82.8	7.7	2051	US-09-962-832-218	Sequence 218, App
15	82.8	7.7	2051	US-09-944-807-20	Sequence 20, Appl
16	82.6	7.6	1065	US-09-922-895-2	Sequence 2, Appl1
17	82.6	7.6	1689	US-09-931-381A-15	Sequence 15, Appl
18	82.6	7.6	1717	US-09-964-824A-100	Sequence 100, App
19	82.6	7.6	1915	US-10-106-623-3	Sequence 3, Appl1

20	82.6	7.6	3426	US-10-001-835-29	Sequence 29, Appl
21	82.4	7.6	1080	US-09-739-151-1	Sequence 1, Appl1
22	82.4	7.6	1102	US-09-870-759-143	Sequence 143, App
23	81.6	7.5	1955	US-10-190-469-2	Sequence 2, Appl1
24	81.6	7.5	2050	US-09-940-240-15	Sequence 15, Appl1
25	77.2	7.1	1083	US-09-852-156-7	Sequence 7, Appl1
26	74	6.8	1895	US-09-940-240-19	Sequence 19, Appl1
27	73.8	6.8	1083	US-09-852-156-11	Sequence 11, Appl1
28	73.4	6.8	1910	US-09-944-807-1	Sequence 1, Appl1
29	73.4	6.8	2080	US-10-044-090-628	Sequence 628, App
30	73.2	6.8	2081	US-10-044-090-627	Sequence 627, App
31	73.2	6.8	1860	US-09-940-240-17	Sequence 17, Appl1
32	72.4	6.7	823	US-10-044-090-598	Sequence 598, App
33	72.4	6.7	993	US-09-826-508-15	Sequence 15, Appl1
34	72.4	6.7	993	US-09-954-456-1129	Sequence 1129, Ap
35	72.4	6.7	1414	US-10-098-841-312	Sequence 312, App
36	71.8	6.6	1892	US-09-900-699A-1	Sequence 1, Appl1
37	71.4	6.6	1563	US-09-880-107-1611	Sequence 1611, Ap
38	70.6	6.5	1083	US-09-852-156-9	Sequence 9, Appl1
39	69.8	6.5	1080	US-09-867-915-2	Sequence 2, Appl1
40	69.8	6.5	2632	US-09-867-915-1	Sequence 3034, Ap
41	69.8	6.5	2632	US-09-867-915-1	Sequence 1, Appl1
42	69.8	6.5	2632	US-09-867-915-26	Sequence 26, Appl
43	69.6	6.4	1014	US-09-791-932-55	Sequence 55, Appl
44	69.6	6.4	1464	US-10-166-359-1	Sequence 1, Appl1
45	69.6	6.4	1464	US-10-166-113-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-943-798-3
; Sequence 3, Application US/09943798
; Patent No. US2002065215A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: OG1021
; CURRENT APPLICATION NUMBER: US/09/943,798
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-798-3

Query Match	93.8%	Score 1014;	DB 10;	Length 1014;
Best Local Similarity	100.0%	Pred. No. 9.2e-291;		
Matches 1014;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	54	ATGATGACCACTAGACTATTATGCAATGCTTCTGATTTCCCGATTATGACGTGCT	113	
DB	1	ATGATGACCACTAGACTATTATGCAATGCTTCTGATTTCCCGATTATGACGTGCT	60	
QY	114	TTTGAAATTTGACCTGATGAAAAATCCCACTCAATGACCTACCTCCCTGTTATTAT	173	
DB	61	TTTGAAATTTGACCTGATGAAAAATCCCACTCAATGACCTACCTCCCTGTTATTAT	120	
QY	174	GGCATATATCTTCCTGCTGGATTTTCCAGGCAATGAGTGTGATTCACCTTACATTTTC	233	
DB	121	GGCATATATCTTCCTGCTGGATTTTCCAGGCAATGAGTGTGATTCACCTTACATTTTC	180	
QY	234	AAATGAGACTTTGGAAGAGACACCATATTATGCTGAACCTGGCTGCACAGATCTG	293	
DB	181	AAATGAGACTTTGGAAGAGACACCATATTATGCTGAACCTGGCTGCACAGATCTG	240	
QY	294	CTGTATCTGACCAAGCTCCCTCTTCTGATTCATCTATGACGATGGCAAACTGGATC	353	
DB	241	CTGTATCTGACCAAGCTCCCTCTTCTGATTCATCTATGACGATGGCAAACTGGATC	300	

; CURRENT APPLICATION NUMBER: US/09/728,422
 ; CURRENT FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: pc_fl_genes Version 2.0
 ; SEQ ID NO 1
 ; LENGTH: 1313
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (547)..(1239)
 ; US-09-728-422-1

Query Match 72.1%; Score 779.4; DB 10; Length 1313;
 Best Local Similarity 99.6%; Pred. No. 4e-221;
 Matches 792; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 CATATTGCCAACTGAACTCTCTTTTCTTGGCAAGTAAAGAGCAACCATGATG 60
 DB 494 CATATTGCCAACTGAACTCTCTTTTCTTGGCAAGTAAAGAGCAACCATGATG 553
 QY 61 AGCCACTAGACTATTAGCAAAATGCTCTGATTTCCCGAATTAGCAGCTTTTGGAA 120
 DB 554 AGCCACTAGACTATTAGCAAAATGCTCTGATTTCCCGAATTAGCAGCTTTTGGAA 613
 QY 121 ATTGCACTGATGAAAATCATCCCACTCAAGATGCACTACCTCCCTGTTATTATGCAATTA 180
 DB 614 ATTGCACTGATGAAAATCATCCCACTCAAGATGCACTACCTCCCTGTTATTATGCAATTA 673
 QY 181 TCTTCTCTGGGATTTCCAGGCAAGTCAAGTATGATATTCATTAATTTCAAAATGA 240
 DB 674 TCTTCTCTGGGATTTCCAGGCAAGTCAAGTATGATATTCATTAATTTCAAAATGA 733
 QY 241 GACCTTGAAGAGCAGACACATATATGCTGAACCTGGCTGACAGATCTGCTGATC 300
 DB 734 GACCTTGAAGAGCAGACACATATATGCTGAACCTGGCTGACAGATCTGCTGATC 793
 QY 301 TGACCAAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGGAAAATGAGATCTTTGGAG 360
 DB 794 TGACCAAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGGAAAATGAGATCTTTGGAG 853
 QY 361 ATTTCATGTGATGTTATTCGCTTCAAGCTTCAATTTCAACCTGTATAGAGCATCTCT 420
 DB 854 ATTTCATGTGATGTTATTCGCTTCAAGCTTCAATTTCAACCTGTATAGAGCATCTCT 913
 QY 421 TCCCTCACTGTTTACAGATCTTCGCTACTGCTGTATCATTCACCAATGAGCTGCTTTT 480
 DB 914 TCCCTCACTGTTTACAGATCTTCGCTACTGCTGTATCATTCACCAATGAGCTGCTTTT 973
 QY 481 CCATTCACAAAATCGATGAGTGTGAGTGAACCTGTGTGTGTGTATCATTTCACTGG 540
 DB 974 CCATTCACAAAATCGATGAGTGTGAGTGAACCTGTGTGTGTGTATCATTTCACTGG 1033
 QY 541 TAGCTGTCAATTCGATGACCTTCTGTATCATTCACCAAGAGCAAGATGAGCTT 600
 DB 1034 TAGCTGTCAATTCGATGACCTTCTGTATCATTCACCAAGAGCAAGATGAGCTT 1093
 QY 601 GTCTGCACTCAACAGTGGATGAATCAATATCTATTAGTGTGTAACCTGATTTTGA 660
 DB 1094 GTCTGCACTCAACAGTGGATGAATCAATATCTATTAGTGTGTAACCTGATTTTGA 1153
 QY 661 CTGCAACTACTTTTCTGCTCCCTTGGTGTATGTGACATTTGCTATACAGATTAATCC 720
 DB 1154 CTGCAACTACTTTTCTGCTCCCTTGGTGTATGTGACATTTGCTATACAGATTAATCC 1211
 QY 721 ACACTTGAACCATGAGCTGCAAACTGACAGCTGCTTAAAGCAAGAAAGCAGAGGCTAA 780
 DB 1212 ACACTTGAACCATGAGCTGCAAACTGACAGCTGCTTAAAGCAAGAAAGCAGAGGCTAA 1271

QY 781 CCATTCTGCTACTCC 795
 DB 1272 CCATTCTGCTACTCC 1286

RESULT 4
 US-09-812-102-40/c
 ; Sequence 40; Application US/09812102
 ; Patent No. US2002005179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Kelch B
 ; TITLE OF INVENTION: No. US2002005179A1 G-Protein Coupled Receptor Homologs
 ; FILE REFERENCE: 5800-41 035800/183478
 ; CURRENT APPLICATION NUMBER: US/09/812,102
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/364,769
 ; PRIOR FILING DATE: 1999-07-30
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40
 ; LENGTH: 526
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: GPCR-RHODOPSIN
 ; US-09-812-102-40

Query Match 47.6%; Score 515; DB 10; Length 526;
 Best Local Similarity 100.0%; Pred. No. 6.3e-143;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 CCTCTCTGATTCATCTATGCAAGTGGGAAAATGAGATCTTTGAGATTTATGATGT 371
 DB 526 CCTCTCTGATTCATCTATGCAAGTGGGAAAATGAGATCTTTGAGATTTATGATGT 467
 QY 372 AAGTTATCGCTGAGCTTCCATTTCAACCTGTATAGAGCATCTCTTCTCACTGT 431
 DB 466 AAGTTATCGCTGAGCTTCCATTTCAACCTGTGTATAGAGCATCTCTTCTCACTGT 407
 QY 432 TTGAGCATCTCCGCTACTGCTGTATTCATCCCAATGAGCTTTTCCATTCACAAA 491
 DB 406 TTGAGCATCTCCGCTACTGCTGTATTCATCCCAATGAGCTTTTCCATTCACAAA 347
 QY 492 ACTGATGTCAGTGTGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
 DB 346 ACTGATGTCAGTGTGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 287
 QY 552 CCGATGACCTTTTGTATCATCAACCAAGAGCAAGAGATGAGCTGTCTGACCTC 611
 DB 286 CCGATGACCTTTTGTATCATCAACCAAGAGCAAGAGATGAGCTGTCTGACCTC 227
 QY 612 ACCAGTGGATGATCACTATATATGATGTAACAACCTGATTTTGAATGCACTACT 671
 DB 226 ACCAGTGGATGATCACTATATATGATGTAACAACCTGATTTTGAATGCACTACT 167
 QY 672 TTCTGCTCCCTTGGATGATGACCTTTGCTATACAGATTAATCAACCTGATACC 731
 DB 166 TTCTGCTCCCTTGGATGATGACCTTTGCTATACAGATTAATCAACCTGATACC 107
 QY 732 CATGACCTGAACTGACAGCTGCTTTAAGCAGAAAGCAGAAAGCTTAACTCTGCTA 791
 DB 106 CATGACCTGAACTGACAGCTGCTTTAAGCAGAAAGCAGAAAGCTTAACTCTGCTA 47
 QY 792 CTCCTTGATTTTATGATGTTTATTTTAACTCTTCA 826
 DB 46 CTCCTTGATTTTATGATGTTTATTTTAACTCTTCA 12

RESULT 5
 US-09-826-791-1
 ; Sequence 1; Application US/09826791
 ; Patent No. US20010039037A1
 ; GENERAL INFORMATION:

TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and

US-09-880-107-2143

Query Match 7.8%; Score 84; DB 10; Length 1670;
Best Local Similarity 49.8%; Pred. No. 8e-15;
Matches 244; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 122 TTGCACTGATGAAACATCCCACTCAAGATGACCTACCTCCCTGTTATTTATGACATTAT 181
DB 156 TTTCGGTGAAGAAATGCTAATTTCAATAAATCTTCTCCCACTCACTACCTCAT 215
QY 182 CTTCCTCGTGGGATTTCCAGGCAATGACATGATGATATCCATTACATTTTCAAAATGAG 241
DB 216 CTTCCTTAAGTGGGATTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 275
QY 242 ACCTTGAAGAGAGACCAATCATTTATGCTGAAGCTGGGCTGACCAAGATTTGCTGATCT 301
DB 276 ACTGAGAACACATGACGACCAAGTACAGGCTGACCTGTCAAGGCGACCTCTCTTTGT 335
QY 302 GACCAAGCTCTCCCTTCTGATCTACTATGACGATGCGGAAACTGATCTTTGAGA 361
DB 336 CATCAAGCTCTCTCTTGGGCACT-----TGATGCCGTGGCAAACTGGTACTTTGGGAA 389
QY 362 TTTCATGATGATTTATTCGCTTCAAGCTTCAATTTCAACTGTATAGACATCTCTT 421
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QY 422 CCTCAAGCTTTTCAAGATCTTCGCTACTGATGATGATGATGATGATGATGATGATGATGAT 481
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QY 482 CATTCACAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
DB 510 GCCAAGAAAGCTGTGGCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
QY 542 AGCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
DB 570 GCTGACTATTCGCACTTCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 629
QY 602 TCTGACCTC 611
DB 630 TGACCGCTTC 639

RESULT 13

US-09-104-063-3
Sequence 3, Application US/09104063
Patent No. US20020168356A1
GENERAL INFORMATION:
APPLICANT: Lee, James
TITLE OF INVENTION: P4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664228

FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-2881
TELEX: 910/571-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-104-063-3

Query Match 7.8%; Score 84; DB 9; Length 1737;
Best Local Similarity 49.8%; Pred. No. 8.2e-15;
Matches 244; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 122 TTGCACTGATGAAACATCCCACTCAAGATGACCTACCTCCCTGTTATTTATGACATTAT 181
DB 174 TTTCGGTGAAGAAATGCTAATTTCAATAAATCTTCTCCCACTCACTACCTCAT 223
QY 182 CTTCCTCGTGGGATTTCCAGGCAATGACATGATGATGATGATGATGATGATGATGATGATGAT 241
DB 234 CTTCCTTAAGTGGGATTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 293
QY 242 ACCTTGAAGAGAGACCAATCATTTATGCTGAAGCTGGGCTGACGATGCTGATCT 301
DB 294 ACTGAGAACACATGACGACCAAGTACAGGCTGACCTGTCAAGTCCGACCTCTCTTTGT 353
QY 302 GACCAAGCTCTCCCTTCTGATCTACTATGACGATGCGGAAACTGATCTTTGAGA 361
DB 354 CATCAAGCTCTCTCTTGGGCACT-----TGATGCCGTGGCAAACTGGTACTTTGGGAA 407
QY 362 TTTCATGATGATTTATTCGCTTCAAGCTTCAATTTCAACTGTATAGACATCTCTT 421
DB 408 CTTCCTATGCAAGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
QY 422 CTTCACCTGTTTCAAGATCTTCGCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 481
DB 468 CTTCGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 527
QY 482 CATTCACAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
DB 528 GCCAAGAAAGCTGTGGCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 587
QY 542 AGCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
DB 588 GCTGACTATTCGCACTTCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 647
QY 602 TCTGACCTC 611
DB 648 TGACCGCTTC 657

RESULT 14

US-09-962-832-218
Sequence 218, Application US/09962832
Patent No. US20020110821A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using S19
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-74

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 06:47:09 (Search time 3443 Seconds)

(without alignments)
7893.996 Million cell updates/sec

Title: US-10-010-568-1

Perfect score: 1081

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1081	100.0	1081	US-60-251-926-1	Sequence 1, Appl1
3	1081	100.0	1081	US-60-269-795-1	Sequence 1, Appl1
4	1081	100.0	9905	US-09-634-656-3	Sequence 3, Appl1
5	1079.4	99.9	1560	US-10-023-634-5	Sequence 5, Appl1
6	1079.4	99.9	1729	US-09-475-790-2	Sequence 2, Appl1
7	1079.4	99.9	1729	US-09-785-2768-24015	Sequence 24015, A
8	1079.4	99.9	1729	US-09-785-2768-25756	Sequence 25756, A
9	1079.4	99.9	1729	US-09-785-2768-29927	Sequence 29927, A
10	1079.4	99.9	43262	US-60-261-974-40	Sequence 30042, A
11	1068.4	98.8	8161	US-60-205-423-233	Sequence 233, App
12	1068.4	98.8	8161	US-60-205-423-234	Sequence 234, App
13	1068.4	98.8	8161	US-60-205-423-235	Sequence 235, App
14	1068.4	98.8	8161	US-60-205-423-236	Sequence 236, App
15	1068.4	98.8	8161	US-60-205-423-237	Sequence 237, App
16	1068.4	98.8	8161	US-60-205-423-238	Sequence 238, App
17	1068.4	98.8	8161	US-60-205-423-239	Sequence 239, App
18	1068.4	98.8	8161	US-60-205-423-240	Sequence 240, App
19	1068.4	98.8	8161	US-60-205-423-241	Sequence 241, App
20	1068.4	98.8	8161	US-60-205-423-242	Sequence 242, App
21	1068.4	98.8	8161	US-60-205-423-243	Sequence 243, App

Db 9336 C 9336

RESULT 5

US-10-023-634-5
; Sequence 5, Application US/10023634
; GENERAL INFORMATION:

APPLICANT: Shimkets, Richard A
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Ballinger, Robert A
APPLICANT: Guo, Xiaojia
APPLICANT: Tchernev, Velizar T
APPLICANT: Shenoy, Sureesh G
APPLICANT: Li, Li
APPLICANT: Ellerman, Karen
APPLICANT: Zerhusen, Bryan D
APPLICANT: Peturajan, Meera
APPLICANT: Caeman, Scacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Gusev, Vladimir Y
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Gangoli, Esha A
APPLICANT: Malyankar, Difel M
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Miller, Isabelle
APPLICANT: Gerlach, Valerie
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-221
CURRENT APPLICATION NUMBER: US/10/023,634
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,025
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/265,163
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,929
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/274,864
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/276,688
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,880
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/286,409
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/309,246
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/315,600
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1560
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-634-5

Query Match 99.9%; Score 1079.4; DB 38; Length 1560;
Best Local Similarity 99.9%; Pred. No. 5.9e-299;
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATATTGCCAACTGAACTCTCTTGTCTTCTGCAAGATGAAGAGACAACCATGATG 60
DB 300 CATATTGCCAACTGAACTCTCTTGTCTTCTGCAAGATGAAGAGACAACCATGATG 359
QY 61 AGCCACTAATCTTTAGCAATGCTTTGATTTCCCGATTATGCAAGCTGCTTTGAA 120
DB 360 AGCCACTAATCTTTAGCAATGCTTTGATTTCCCGATTATGCAAGCTGCTTTGAA 419
QY 121 ATTGACGTATGAAGAAATCCCACTCAAGATGACATACCTCCTGTTATTATGACATTA 180

DB 420 ATTGACGTATGAAGAAATCCCACTCAAGATGACATACCTCCTGTTATTATGACATTA 479
QY 181 TCTTCTGCTGGGATTTCCAGCAATGACATGATGATATCCATTACATTTTCAAAATGA 240
DB 480 TCTTCTGCTGGGATTTCCAGCAATGACATGATGATATCCATTACATTTTCAAAATGA 539
QY 241 GACCTTGAAGAGACACATCATTTATAGCTGAACCTGGCTGCAAGATCTGCTATG 300
DB 540 GACCTTGAAGAGACACATCATTTATAGCTGAACCTGGCTGCAAGATCTGCTATG 599
QY 301 TGACGACCTCCCTCCGATTTCACTATAGCCAGTGGCCAAAATGATCTTTGAG 360
DB 600 TGACGACCTCCCTCCGATTTCACTATAGCCAGTGGCCAAAATGATCTTTGAG 659
QY 361 ATTGATGTATGATTTATCCGCTTCACTTCACTTCAACCTGTATAGAGATCTCT 420
DB 660 ATTGATGTATGATTTATCCGCTTCACTTCACTTCAACCTGTATAGAGATCTCT 719
QY 421 TCTTCACTGTTTCAAGCATCTTCCGCTATCTGTATCATTCACCAATGAGCTGCTT 480
DB 720 TCTTCACTGTTTCAAGCATCTTCCGCTATCTGTATCATTCACCAATGAGCTGCTT 779
QY 481 CCATTCAAGAAATGATGTGATGATTTAGCTGTGCTGTGTGTGATCATTTCACTGG 540
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QY 541 TAGCTGTATTCAGATGACCTTCTTGATCATCAATCAACCAAGAGCCATGACCT 600
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QY 601 GTCTGACCTTCAAGCATCTTCCGCTGTGTATGATGACATTTGCTATACCAATATTC 660
DB 900 GTCTGACCTTCAAGCATCTTCCGCTGTGTATGATGACATTTGCTATACCAATATTC 959
QY 661 CTGCACTACTTCTGCTCTCCCTGTGTATGATGACATTTGCTATACCAATATTC 720
DB 960 CTGCACTACTTCTGCTCTCCCTGTGTATGATGACATTTGCTATACCAATATTC 1019
QY 721 AACCTGACCTTCAAGCATCTTCCGCTGTGTATGATGACATTTGCTATACCAATATTC 780
DB 1020 AACCTGACCTTCAAGCATCTTCCGCTGTGTATGATGACATTTGCTATACCAATATTC 1079
QY 781 CCATTCTGATCTCTGATTTATAGTATTTTACCTTCAATCTTGAAGGCTCA 840
DB 1080 CCATTCTGATCTCTGATTTATAGTATTTTACCTTCAATCTTGAAGGCTCA 1139
QY 841 TTGCGATGATCTGCGCTGTTCAATGATTTTCATTGATGATGATCCATGAG 900
DB 1140 TTGCGATGATCTGCGCTGTTCAATGATTTTCATTGATGATGATCCATGAG 1199
QY 901 CTTACATCGTTTCAAGCAATGATGCTGTGAAACCTTTGTTGTTACTATATG 960
DB 1200 CTTACATCGTTTCAAGCAATGATGCTGTGAAACCTTTGTTGTTACTATATG 1259
QY 961 TGTGTGACGACCACTTCAAGAGCTGTGTCAAGAGATGCAAAATGAAAGCG 1020
DB 1260 TGTGTGACGACCACTTCAAGAGCTGTGTCAAGAGATGCAAAATGAAAGCG 1319
QY 1021 GAAACCTTGAAGCAAGAAATATGTTACTCAAAACCTTGAATTTTCAATTA 1080
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DB 1380 C 1380

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; Sequence 2, Application US/09475790
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra

QY 121 ATTGACGTGATGAAAAATCCCACTGCAAGATGACTACCTCCCTGTTATTTATGAGCTTA 180
 Db 361 ATTGACGTGATGAAAAATCCCACTGCAAGATGACTACCTCCCTGTTATTTATGAGCTTA 420
 QY 181 TCTTCTGCTGGGATTTTCCAGGCAATGCAAGTATGATTCACCTTATTTTCAAAAATGA 240
 Db 421 TCTTCTGCTGGGATTTTCCAGGCAATGCAAGTATGATTCACCTTATTTTCAAAAATGA 480
 QY 241 GACCTTGAAGAGAGACCAATCATATATGCTGAACCTGGCTGCAAGATCTGCTATTC 300
 Db 481 GACCTTGAAGAGAGACCAATCATATATGCTGAACCTGGCTGCAAGATCTGCTATTC 540
 QY 301 TGACCAAGCTCCCTTCCCTGATTTCACTATATGCGAGGCGCAAACTGGATCTTTGAG 360
 Db 541 TGACCAAGCTCCCTTCCCTGATTTCACTATATGCGAGGCGCAAACTGGATCTTTGAG 600
 QY 361 ATTTCATGTATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGTATAGAGCATCTCT 420
 Db 601 ATTTCATGTATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGTATAGAGCATCTCT 660
 QY 421 TCCCTCACTGTTTTCAGCATCTTCCTGCTATGATTCATTCACCAATGAGCTGCTTTT 480
 Db 661 TCCCTCACTGTTTTCAGCATCTTCCTGCTATGATTCATTCACCAATGAGCTGCTTTT 720
 QY 481 CCATTCACAAAATCGATGTGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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 Db 781 TAGCTGTATTCGATGACCTTCTTGATCATCAACAAGAGCAACATGACGCT 840
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 Db 1261 GGAACCTTGAAGAGCAAAAGAAATTAATTAATCAACACCTTGAATATATTTCAATTA 1320
 QY 1081 C 1081
 Db 1321 C 1321

RESULT 8
 US-09-785-276A-25756
 ; Sequence 25756, Application US/09785276A

GENERAL INFORMATION:
 APPLICANT: Schlegel, Robert
 APPLICANT: Endege, Wilson
 APPLICANT: Monahan, John
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 TITLE OF INVENTION: HUMAN PROSTATE CANCER
 FILE REFERENCE: MRI-007B
 CURRENT APPLICATION NUMBER: US/09/785,276A
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: 60/183,319
 PRIOR FILING DATE: 2000-02-17
 PRIOR APPLICATION NUMBER: 60/189,862
 PRIOR FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/207,454
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/211,314
 PRIOR FILING DATE: 2000-06-09
 PRIOR APPLICATION NUMBER: 60/219,007
 PRIOR FILING DATE: 2000-07-18
 PRIOR APPLICATION NUMBER: 60/255,281
 PRIOR FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 62232
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 25756
 LENGTH: 1729
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURES:
 NAME/KEY: misc_feature
 LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17
 OTHER INFORMATION: n = A,T,C or G
 US-09-785-276A-25756

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Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 541 TGACCAAGCTCCCTTCCCTGATTTCACTATATGCGAGGCGCAAACTGGATCTTTGAG 600
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 Db 601 ATTTCATGTATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGTATAGAGCATCTCT 660
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 Db 1261 GGAACCTTGAGCAAGCAAGAAATAGTATCTCAACAAACCTTGAAATATTTCAATTA 1320
 Oy 1081 C 1081
 Db 1321 C 1321

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 ; Sequence 30042, Application US/09785276A
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; FILE REFERENCE: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: NRI-007B
 ; CURRENT APPLICATION NUMBER: US/09/785,276A
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30042
 ; LENGTH: 1729
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-785-276A-30042

Query Match 99.9%; Score 1079.4; DB 30; Length 1729;
 Best Local Similarity 99.9%; Pred. No. 6.2e-299;
 Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 CATATTGCCAACTGAATCTCTCTTTTCTTGCAAGATGAAGAGACCAACATGATG 60
 Db 241 CATATTGCCAACTGAATCTCTCTTTTCTTGCAAGATGAAGAGACCAACATGATG 300
 Oy 61 AGCCACTAGACTATTAGCAAAATGCTTGTATTTCCCGCATTTAGCAGCTGCTTTGAA 120
 Db 301 AGCCACTAGACTATTAGCAAAATGCTTGTATTTCCCGCATTTAGCAGCTGCTTTGAA 360
 Oy 121 ATTGACTGATGAAAACATCCCACTCAAGTGAATGACCTCCCTGTTATTATGAGATTA 180
 Db 361 ATTGACTGATGAAAACATCCCACTCAAGTGAATGACCTCCCTGTTATTATGAGATTA 420
 Oy 181 TCTTCTGTGGGATTTCCAGGCAATGAGTATGATGATTCACCTTCAATTTCAAAATGA 240
 Db 421 TCTTCTGTGGGATTTCCAGGCAATGAGTATGATGATTCACCTTCAATTTCAAAATGA 480
 Oy 241 GACCTGGAAGGACGACCATCATTTATGCTGAACCTGGCTTGACAGATCTGCTGATC 300

Db 481 GACCTGGAAGGACGACCATCATTTATGCTGAACCTGGCTTGACAGATCTGCTGATC 540
 Oy 301 TGACCAAGCTCCCTCTCTCTGATTTCACTATATGACAGTGGCGAAAATGATCTTTGAG 360
 Db 541 TGACCAAGCTCCCTCTCTCTGATTTCACTATATGACAGTGGCGAAAATGATCTTTGAG 600
 Oy 361 ATTTCAATGATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGTATGAGAGATCTCT 420
 Db 601 ATTTCAATGATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGTATGAGAGATCTCT 660
 Oy 421 TCTTCACTGTTTCAAGATCTCCGCTACCTGTATGATTTCAATCCCATATGAGCTCTTT 480
 Db 661 TCTTCACTGTTTCAAGATCTCCGCTACCTGTATGATTTCAATCCCATATGAGCTCTTT 720
 Oy 481 CCATTCACAAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 721 CCATTCACAAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 Oy 541 TACCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 781 TACCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Oy 601 GTCGACCTGACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Db 841 GTCGACCTGACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Oy 661 CTGCAACTACTTTCGCTCCCTGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Db 901 CTGCAACTACTTTCGCTCCCTGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Oy 721 ACACCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 Db 961 ACACCTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Oy 781 CCATTCGCTACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Db 1021 CCATTCGCTACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Oy 841 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Db 1081 TTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 Oy 901 CTTCATGCTTTTCAACCATTTAGCTGCTGAACACCTTGTGTAACCTGTTACTATGAT 960
 Db 1141 CTTCATGCTTTTCAACCATTTAGCTGCTGAACACCTTGTGTAACCTGTTACTATGAT 1200
 Oy 961 TGGTGTGACGACCACTTTACAGAGGCTGTCTGCTCAACAGTGAAGTGAAGTGAAGC 1020
 Db 1201 TGGTGTGACGACCACTTTACAGAGGCTGTCTGCTCAACAGTGAAGTGAAGTGAAGC 1260
 Oy 1021 GGAACCTTGAGCAAGCAAGAAATAGTATCTCAACAAACCTTGAAATATTTCAATTA 1080
 Db 1261 GGAACCTTGAGCAAGCAAGAAATAGTATCTCAACAAACCTTGAAATATTTCAATTA 1320
 Oy 1081 C 1081
 Db 1321 C 1321

RESULT 11
 US-60-261-974-40
 ; Sequence 40, Application US/60261974
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
 ; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: C1001096-PROV
 ; CURRENT APPLICATION NUMBER: US/60/261,974
 ; NUMBER OF SEQ ID NOS: 237
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40

180

RESULT 14
US-60-205-423-235
; Sequence 235, Application US/60205423
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

Search completed: January 30, 2003, 09:39:16
Job time : 3519 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 06:06:20 ; Search time 872 Seconds
(without alignments)
1406.854 Million cell updates/sec

Title: US-10-010-568-1
Perfect score: 1081
Sequence: 1 catatgccaaactgacac.....ccttgaatttcattac 1081

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2475311 seqs, 567426730 residues

Total number of hits satisfying chosen parameters: 4950622

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New:*
1: /cgn2_6/prodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/prodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/prodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/prodata/1/pna/US08_NEW_COMB.seq:*
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6: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1081	100.0	1414	6	US-10-017-161-525
2	1081	100.0	9905	6	US-10-270-144-3
3	1014	93.8	1014	6	US-10-270-144-1
4	1014	93.8	1014	6	US-10-188-405-7
5	1014	93.8	1014	6	US-10-321-807-27
6	1012.4	93.7	1014	6	US-10-278-141-10
7	1012.4	93.7	1014	6	US-10-278-107-33
8	1012.4	93.7	1014	6	US-10-296-081-10
9	479.8	44.4	545	6	US-10-276-774-102
10	134.4	12.4	1428	6	US-10-270-857-1
11	134.4	12.4	1428	6	US-10-270-587-1
12	134.2	12.4	3055	6	US-10-305-720-1456
13	131.2	12.1	1005	6	US-10-272-983-35
14	131.2	12.1	1436	6	US-10-264-237-1352
15	131.2	12.1	1436	6	US-10-311-671-20
16	123	11.4	1429	6	US-10-305-720-1068
17	107.8	10.0	2025	5	US-09-814-915A-74
18	107.8	10.0	2025	5	US-10-305-720-1482
19	100	9.3	984	5	US-09-461-436B-41
20	97.4	9.0	1571	6	US-10-305-720-1108
21	95.8	8.9	984	5	US-09-461-436B-57
22	94.4	8.7	1428	6	US-10-152-319A-2045
23	93.6	8.7	1041	6	US-10-278-107-35
24	93.6	8.7	1041	6	US-10-321-807-13
25	93.6	8.7	1041	6	US-10-321-807-87
26	93.6	8.7	2807	5	US-09-879-603A-1

27	93.6	8.7	2807	5	US-09-979-603-1	Sequence 1, Appli
28	90.8	8.4	1900	6	US-10-305-720-1484	Sequence 1464, Ap
29	90.8	8.4	2070	1	PCT-US02-29560-44	Sequence 44, Appl
30	90.8	8.4	2070	6	US-10-245-882-44	Sequence 2068, Ap
31	90.4	8.4	1922	6	US-10-152-319A-2068	Sequence 35, Appl
32	87.6	8.1	1092	6	US-10-321-807-35	Sequence 511, App
33	87.6	8.1	1192	6	US-10-017-161-511	Sequence 765, App
34	87.6	8.1	5015	6	US-10-017-161-765	Sequence 807, Appl
35	87.6	8.1	8367	6	US-10-017-161-807	Sequence 21, Appl
36	87.2	8.1	2409	5	US-09-360-482B-21	Sequence 46, Appl
37	84	7.8	1059	6	PCT-US02-29560-46	Sequence 45, Appl
38	84	7.8	1059	6	US-10-245-882-46	Sequence 1235, Ap
39	84	7.8	1225	7	US-10-305-720-1235	Sequence 317, Appl
40	84	7.8	1670	7	US-60-427-982-117	Sequence 807, Appl
41	84	7.8	1679	1	PCT-US02-04915-80	Sequence 332, App
42	84	7.8	1679	6	US-10-170-385-332	Sequence 9205, Ap
43	84	7.8	1679	6	US-10-325-899-9205	Sequence 1, Appli
44	83.8	7.8	1451	5	US-09-958-805A-1	Sequence 19, Appl
45	83.8	7.8	1451	5	US-09-360-482B-19	

ALIGNMENTS

RESULT 1
US-10-017-161-525
Sequence 525, Application US/10017161
GENERAL INFORMATION:

APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABRUANT, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017, 161
PRIOR APPLICATION NUMBER: 2002-12-18
PRIOR FILING DATE: 2001/246789
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 525
LENGTH: 1414
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(1414)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(1214)
US-10-017-161-525

Query Match 100.0%; Score 1081; DB 6; Length 1414;
Best Local Similarity 100.0%; Pred. No. 8.4e-295;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CATATGCCAACTGAACTCTCTGTTTCTTGGAAGTGAAGGAACAACCATGATG	60
DB	148	CATATGCCAACTGAACTCTCTGTTTCTTGGAAGTGAAGGAACAACCATGATG	207
QY	61	AGGCACAGTGAATTTAGCAAAATGCTTCTGATTTCCCGATTTATGACAGTCTTTGGAA	120
DB	208	AGGCACAGTGAATTTAGCAAAATGCTTCTGATTTCCCGATTTATGACAGTCTTTGGAA	267
QY	121	ATTGCACTATGAAATCATCTCCACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	180
DB	268	ATTGCACTATGAAATCATCTCCACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	327
QY	181	TCTTCCTCGGGATTTCCAGGAATGAGTGAATGATGATGATGATGATGATGATGATGATG	240
DB	328	TCTTCCTCGGGATTTCCAGGAATGAGTGAATGATGATGATGATGATGATGATGATGATG	387
QY	241	GACCTTGAAGAGCAGACATCATATATGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	300

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Db 9156 CTTACATCGTTTCTAGACCATTTAGTCTGTGAAACCTTTGGTAACCTGTATTACTATATG 9215
Qy 961 TGGTGTGACGACCACTTTTCAAGAGGCTGTCTGTAAACGTAGATGCAAGTAAGACG 1020
Db 9216 TGGTGTGACGACCACTTTTCAAGAGGCTGTCTGTAAACGTAGATGCAAGTAAGACG 9275
Qy 1021 GGAACCTTGACGACCAAGAAATTTAGTACTGAAACCAACCTTTGAAATTTTCAATTA 1080
Db 9276 GGAACCTTGACGACCAAGAAATTTAGTACTGAAACCAACCTTTGAAATTTTCAATTA 9335
Qy 1081 C 1081
Db 9336 C 9336

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RESULT 3

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US-10-270-144-1
; Sequence 1, Application US/10270144
; GENERAL INFORMATION:
; APPLICANT: MEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NOCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-1

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Query Match 93.8%; Score 1014; DB 6; Length 1014;

Best Local Similarity 100.0%; Pred. No. 5.9e-276;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 54 ATGAATGAGCCACTAGACTATTGGAATATGCTTGTGATTTCCCGCATTAAGAGCTGCT 113
Db 1 ATGAATGAGCCACTAGACTATTGGAATATGCTTGTGATTTCCCGCATTAAGAGCTGCT 60
Qy 114 TTGGAATGACATGATGATAAAATCCCACTCAAGATGACATCACTCCCTGTTATTTAT 173
Db 61 TTGGAATGACATGATGATAAAATCCCACTCAAGATGACATCACTCCCTGTTATTTAT 120
Qy 174 GGCATTATTTCTCTGTGGATTTTCAAGGCAATGCAATGATGATTCATTAATTTTC 233
Db 121 GGCATTATTTCTCTGTGGATTTTCAAGGCAATGCAATGATGATTCATTAATTTTC 180
Qy 234 AAAATGAGACTTGGAAAGAGACCAATCATATATGCTAACTGGCCCTGCAAGATTCG 233
Db 181 AAAATGAGACTTGGAAAGAGACCAATCATATATGCTAACTGGCCCTGCAAGATTCG 240
Qy 234 CTGATCTGACAGCCTCCCTTCTGATTCATCTATATGCAAGTGGCAAACTGATC 353
Db 241 CTGATCTGACAGCCTCCCTTCTGATTCATCTATATGCAAGTGGCAAACTGATC 300
Qy 354 TTGGAATGATTCATGATGATTTATCCGCTTCAAGCTTCATTTCAACCTGATATAGAC 413
Db 301 TTGGAATGATTCATGATGATTTATCCGCTTCAAGCTTCATTTCAACCTGATATAGAC 360
Qy 414 ATCCCTTCTCAACCGTTTGTAGCATCTCCGCTAGTGTATCATTTTCAACCAATGAGC 473
Db 361 ATCCCTTCTCAACCGTTTGTAGCATCTCCGCTAGTGTATCATTTTCAACCAATGAGC 420
Qy 474 TGCCTTTTCCATTCACAAATCGATGTGAGTGTAGCCGTGTGTGTGTGTGTGTGTGT 533
Db 421 TGCCTTTTCCATTCACAAATCGATGTGAGTGTGTAGCCGTGTGTGTGTGTGTGTGTGT 480

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Qy 534 TCACGTGAGCTGTGCATTTCCGATAGACCTTTCTTGATCAGATCAACCAAGGACCAACGA 593
Db 481 TCACGTGAGCTGTGCATTTCCGATAGACCTTTCTTGATCAGATCAACCAAGGACCAACGA 540
Qy 594 TCACGTGAGCTGTGCATTTCCGATAGACCTTTCTTGATCAGATCAACCAAGGACCAACGA 653
Db 541 TCACGTGAGCTGTGCATTTCCGATAGACCTTTCTTGATCAGATCAACCAAGGACCAACGA 600
Qy 654 ATTTGACGTGACATCTATTTCTGCTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 713
Db 601 ATTTGACGTGACATCTATTTCTGCTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Qy 714 ATTATCCACTCTGACCTCAACCTGACATGCACTGCAACCTGCTTAAAGCAAAAGACGA 773
Db 661 ATTATCCACTCTGACCTCAACCTGACATGCACTGCAACCTGCTTAAAGCAAAAGACGA 720
Qy 774 AGGCTAACCAATTCGTCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 833
Db 721 AGGCTAACCAATTCGTCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 780
Qy 834 AGGCTAACCAATTCGTCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 893
Db 781 AGGCTAACCAATTCGTCTACTCTGCTGATTTTACGTAATTTTACCTTCCATATCTTG 840
Qy 894 CATGAACCTTACATCTGTTTCTGACCAATTAAGCTGTCTGAAACCTTTGTGTAACCTGTTA 953
Db 841 CATGAACCTTACATCTGTTTCTGACCAATTAAGCTGTCTGAAACCTTTGTGTAACCTGTTA 900
Qy 954 CTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1013
Db 901 CTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
Qy 1014 GTAAGCGGAACTTGTGACGACCAAGAAATTTAGTACTCAAAACCAACCTTGA 1067
Db 961 GTAAGCGGAACTTGTGACGACCAAGAAATTTAGTACTCAAAACCAACCTTGA 1014

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RESULT 4

US-10-188-405-7

; Sequence 7, Application US/10188405

; GENERAL INFORMATION:

; APPLICANT: Tian, Hui

; APPLICANT: Dai, Kang

; APPLICANT: Chen, Jin-Long

; APPLICANT: Zhao, Jiaqiang

; APPLICANT: Cutler, Gene

; APPLICANT: Tularik Inc.

; TITLE OF INVENTION: Novel Receptors

; FILE REFERENCE: 018781-008410US

; CURRENT APPLICATION NUMBER: US/10/188,405

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: US 60/302,800

; PRIOR FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 1014

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human TGR164

US-10-188-405-7

Query Match 93.8%; Score 1014; DB 6; Length 1014;

Best Local Similarity 100.0%; Pred. No. 5.9e-276;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 54 ATGAATGAGCCACTAGACTATTGGAATATGCTTGTGATTTCCCGCATTAAGAGCTGCT 113
Db 1 ATGAATGAGCCACTAGACTATTGGAATATGCTTGTGATTTCCCGCATTAAGAGCTGCT 60
Qy 114 TTGGAATGACATGATGATAAAATCCCACTCAAGATGACATCACTCCCTGTTATTTAT 173

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894 CATGAGCTTACATCGTTTCTAGACCATAGCGTCTGAAACCTTGGTAACTGTTA 953
841 CATGAGCTTACATCGTTTCTAGACCATAGCGTCTGAAACCTTGGTAACTGTTA 900

954 CTATATGTGGTGTACGCAACATTTCAGAGGCTGTCTGCTCAACAGTCAGATGCAAA 1013


```

APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: GRAUD, Richard
APPLICANT: KHAN, Farrah A.
APPLICANT: GANDHI, Ameena R.
APPLICANT: WALIA, Narinder K.
APPLICANT: NGUYEN, Damien B.
APPLICANT: YUE, Henry
APPLICANT: HAFALIA, April
APPLICANT: ELIOTT, Vicki S.
APPLICANT: LAL, Preeti
APPLICANT: REDDY, Roopa
APPLICANT: KALICK, Deborah A.
APPLICANT: TANG, Y. Tom
APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096 PCT
CURRENT FILING DATE: 2002-11-18
PRIOR FILING DATE: 2000-05-16; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 6575963CB1
US-10-296-081-10

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Query Match          93.7%; Score 1012.4; DB 6; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.7e-275;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 54 ATGATGAGGCACTAGATATTTAGCAATGCTTCTGATTTCCCGGATTTAGCAGCTGCT 113
DB 1 ATGATGAGGCACTAGATATTTAGCAATGCTTCTGATTTCCCGGATTTAGCAGCTGCT 60
QY 114 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGACACTCCCTGTTATTTAT 173
DB 61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGACACTCCCTGTTATTTAT 120
QY 174 GGCAATATCTTCTCGTGGATTTCCAGGCAATGCACTGATGATATCACTTATTTTC 233
DB 121 GGCAATATCTTCTCGTGGATTTCCAGGCAATGCACTGATGATATCACTTATTTTC 180
QY 234 AAAATAGACCTTGAAGAGACAGACATATTTGCTGAACCTGCTGACAGATCTG 293
DB 181 AAAATAGACCTTGAAGAGACAGACATATTTGCTGAACCTGCTGACAGATCTG 240
QY 294 CTGATCTGACAGGCTCCCTCTCTGATTCACCTACTATGCGAGTGGCGAAACTGGATC 353
DB 241 CTGATCTGACAGGCTCCCTCTCTGATTCACCTACTATGCGAGTGGCGAAACTGGATC 300
QY 354 TTGGAGATTCATGATGATTTATCGGCTTCACTTCACTGATGATGAGC 413
DB 301 TTGGAGATTCATGATGATTTATCGGCTTCACTTCACTGATGATGAGC 360
QY 414 ATCCCTCTCCTACCGCTTTGACGATTTCCGTTACTGTTGATTCATTCACCCATGAGC 473
DB 361 ATCCCTCTCCTACCGCTTTGACGATTTCCGTTACTGTTGATTCATTCACCCATGAGC 420
QY 474 TGCCTTTTCATTCACAAACTGATGATGATTTAGCTGCTGCTGCTGCTGATTCATT 533
DB 421 TGCCTTTTCATTCACAAACTGATGATGATTTAGCTGCTGCTGCTGCTGATTCATT 480
QY 534 TCACTGATGATGATTCATTCGATGATCTTTGATTCATTCACCAAGAGCAAGCAAGA 593
DB 481 TCACTGATGATGATTCATTCGATGATCTTTGATTCATTCACCAAGAGCAAGCAAGA 540
QY 594 TCAAGCCTGCTGACCTGACAGATTTGATGATGATTAATTAATGATGATGATGATGAT 653

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DB 541 TCAAGCCTGCTGACCTGACCAAGTTGGATGATTAATTAATGATGATGATGATGAT 600
QY 654 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713
DB 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 714 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773
DB 661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 774 AGGCTTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
DB 721 AGGCTTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 834 AGGCTTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893
DB 781 AGGCTTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 894 CATGAAGCTTACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 953
DB 841 CATGAAGCTTACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 954 CATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013
DB 901 CATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 1014 GTPAAGCGGGAACCTTGAGCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAAT 1067
DB 961 GTPAAGCGGGAACCTTGAGCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAAT 1014

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RESULT 9
US-10-276-774-102/c
Sequence 102, Application US/10276774
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT FILING DATE: 2002-11-18
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 102
LENGTH: 545
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(545)
OTHER INFORMATION: n = a, t, c or g
US-10-276-774-102

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Query Match          44.4%; Score 479.8; DB 6; Length 545;
Best Local Similarity 98.7%; Pred. No. 2e-125;
Matches 526; Conservative 0; Mismatches 2; Indels 5; Gaps 4;

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Db 176 TTTTATGGAGTATGAGTTCGTTGGAGATCTTGGAAATACATGTTGTTTACGGCTAC 235
Qy 228 ATTTTCAAAATGAGACCTTGGAGAGACGACCATTAATGCTGAACCTGGCTGACA 287
Db 236 ATCTTCTCTGAAAGAACTGGAACAGCATTAATTTATCTTTAACTCTCTGCTCT 295
Qy 288 GATCTGCTATATGACAGCCTCCCTTCTGATTCATCTACTATGACGAGGGGAAAC 347
Db 296 GATTAAGCTTTTCTGACACCTCCCAATGCTATAGAGGTTATGCAATG--AAAC 352
Qy 348 TGGATCTTGGAGATTTCAATGCTAATGCTTATCCGCTTCAAGCTTCAATTTCACTGAT 407
Db 353 TGGATATATGAGAGAGCTGCTGACATAGACACGATATGCTTATATGCAACTCTAT 412
Qy 408 AGCAGATCTCTCTCTCACTGTTTCAAGATTTCCGCTACTGCTGATCATTCACCA 467
Db 413 ACCAGCATCTCTCTCTCACTTATTCAGATATGATGATGATGATGATGATGATGAT 472
Qy 468 ATGAGCTGCTTTTCCATTCACAAAATCGATGCTGAGTGTGAGCCGCTGCTGCTGCTG 527
Db 473 TTTCCGAGAACACTTCTGCAAAAAGAGTGTGCTATTTTAACTCTTGGCCATGCTG 532
Qy 528 ATCATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 587
Db 533 GTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
Qy 588 AACAGATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 647
Db 593 AATGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652
Qy 648 AACCTGATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 707
Db 653 AGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Qy 708 ACCAGATTTT-----ATCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761
Db 713 TACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772
Qy 762 CAGAAAGCAGAGAGGCTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 821
Db 773 GAAAAGCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
Qy 822 TTCCATATTTGAGGCTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875
Db 833 TATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892
Qy 876 TCCATTTGAGATCAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 935
Db 893 TGCATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
Qy 936 ACCTTGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
Db 953 AGGTGATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996

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RESULT 12
 US-10-305-720-1456
 ; Sequence 1456, Application US/10305720
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
 ; FILE REFERENCE: PA-0002-1-CON
 ; CURRENT APPLICATION NUMBER: US/10/305,720
 ; PRIOR FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: 09/016,434
 ; NUMBER OF SEQ ID NOS: 1490
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1456
 ; LENGTH: 3055
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

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NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No: 9798835
US-10-305-720-1456

Query Match      12.4%; Score 134.2; DB 6; Length 3055;
Best Local Similarity 50.1%; Pred. No. 1e-27;
Matches 424; Conservative 0; Mismatches 408; Indels 15; Gaps 3;

Qy 145 TCAAGATGCACTACCTCCCTGTTATTTATGAGCATTTATCTTCCCTGAGGATTTCCAGCA 204
Db 995 TCCAGTTTACTACTGCGCGCTGCTACATCTTGTATTCATCATCGCTTCTCTGCGCA 1054
Qy 205 ATGCACTAGTATGATTCATCTTACATTTTCAAAATGAGACCTTGGAGAGAGACCATCA 264
Db 1055 AAGCGTGGCCATCTGAGATGTTGCTTCCACATGAAAGCCCTGAGCGGATCTCGGT 1114
Qy 265 TTATGCTGAACCTGGCGCTGACAGATCTGCTGATTTGACAGCCCTCCCTTCTGATTC 324
Db 1115 ACATGTTCAATTTGGCTCTGCGCACTTCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1174
Qy 325 ACTATATGCAAGTGGCGAAATCTGATCTTGTGAGATTTCAATGCTTATTCGCT 384
Db 1175 TCTACTACTTGAATTAACAGCTGATCTTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
Qy 385 TCAAGTTCAATTTCACTGCTGATGAGACATCTCTCTCACTGCTGCTGCTGCTGCTGCTGCT 444
Db 1235 TCACTTTCAATGATGATCTCTAT--GGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1291
Qy 445 GCTACTGCTGATCATTCACCAATGAGCTGCTTTCATTCACAAAATCGATGCTGAG 504
Db 1292 GGTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
Qy 505 TTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
Db 1352 TCTGATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1411
Qy 563 -CTTGAATCAATCAACCAAGAGCAACAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
Db 1412 ACTCAGGTCACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1471
Qy 622 ATGAATCAATCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
Db 1472 AGTACCTGCAAGTATTTATCTATCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1531
Qy 682 CTTTGTGATGATGACATCTTGTATACCAATTTTCAACTCTGCTGCTGCTGCTGCTGCTGCTGCT 741
Db 1532 CTTTGTGCTGATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1591
Qy 742 AAATGACAGCTGCTTAAAGCAAGAAAGCAAGGCTAACATCTGCTGCTGCTGCTGCTGCTGCT 801
Db 1592 TGGACAACTCTCTGAGAGAAATGATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1651
Qy 802 TTATGCTATTTTATTTTACCTTTCATCTGATGAGGCTCATTCGATGCAATCTGCTGCTGCT 861
Db 1652 TTGCTGTGCTTCAATCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1711
Qy 862 TTT-----CAATGCTGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
Db 1712 ATTTTCAACCCCAAGCAATGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1771
Qy 913 CTAGACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
Db 1772 CAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1831
Qy 973 ACAACTT 979
Db 1832 ATACTTT 1838

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RESULT 13
 US-10-272-983-35
 ; Sequence 35, Application US/10272983
 ; GENERAL INFORMATION:

[illegible]

Query Match	Best Local Similarity	12.11	Score 131.2	DB 6	Length 1542
Matches 436	Conservative 0	Mismatches 433	Indels 15	Gap	
Qy	108	GCTGCTTTGGAAATTTGACATGATGAAACAATCCCACTCAAGATGACACTACCTCCCTGT	1		
Db	222	GCAACTTGCAAAAACCTGCTGGCAGCAGAGAGCTGCCCTCGAAAAAGTACTACTTTCCATT	2		
Qy	168	ATTATGGCATTATCTTCTCGTGGGATTTCCAGGGCAATGCAATGATGATATCCACTTAC	2		
Db	282	TTTTATGGAGATGAGTTGCTGGTGGAGTCTTGAAAAATCACTGTGTGTTACGGCTAC	3		
Qy	228	ATTTTCAAATGAGACCTTGGAAAGACAGACCAATCATTTATGCTGAACCTGGCTGACA	28		
Db	342	ATCTTCTCTGGAAGACGGAACACAGTAATATTATCTTTTAACCTCTCTGCTCT	40		
Qy	288	GATCTGCTGATATGACCAAGCCCTCCCTCTGATTCACACTACTATAGCCAGTGGCAAAAC	34		
Db	402	GACTTAGCTTTCTGTGGACCCCTCCCAATGCTGATAGAGATTATGCAATGG---AAAC	45		
Qy	348	TGATCTTTGGAGATTTCAATGTGTAAGTTTATCCGCTCAGCTTCATTTCACCTGTAT	40		
Db	459	TGGATATATGAGAGCGTGTCTGCAATAGCAACCGATATGTGCTTCATAGCAACCTGTAT	51		
Qy	408	AGAGATCTCTTCTCTCACTGTTTCAGCATCTTCCGCTACTGTGATATCATTCACCA	46		
Db	519	ACCAAGATTTCTTCTCACTTTATGAGCAATATGATATCTTGATATTTAATATCTCT	57		
Qy	468	ATGAGCTGCTTTCCATTCACAAAACCTGATGAGTGCAGTTGAGCTGTGGTGTGG	52		
Db	579	TTCCGAGAACACCTTCTGCAAAAAGAGAGTTGCTATTTTAATCTCCTGGCAATTGG	63		
Qy	528	ATCATTTGACTGTAGCTGATTCGCGATGACCTTGTGATACATCAACCAAGGACC	58		
Db	639	GTTTATGTAACCTTAGAGTTACTACCAATCTTCCCTTTAAATCTGTTATATGAC	69		
Qy	588	AAACGATCAAGCTGTCTGACCTCACAGATCGGATGAATCAATACATTAATAGTGTAC	64		
Db	699	AATGGACCAACCTGTATATGATTTGCAAGTTCTGGAGACCCCACTACACACTCATTTAC	75		
Qy	648	AACCTGATTTTGAAGTGAACACTCTTCTGCTCCCTGGTGTATGACACTTGTCTAT	70		
Db	759	AGCATGTCTTAACCTGTTGGGGTCTCTATTTCTCTTTTGTGATGTGTTCTTTTAT	81		

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2y 708 ACCGCGAT-----ATCGACACTCTGACCCGATGAGCTGCAAACTGACAGCTGCTTAAG 761
db 819 TACAGATGCTCTCTCTCTTAAGCAGAGATAGGAGGTTGCTACTGCTCTGCCCCCTT 878
2y 762 CAGAAAGCAGAGAGGCTAACCATTCCTGCTACTCTCTGCAATTTTAACTATGTTTTTACC 821
db 879 GAAAGGCTCTCAACTTGGTATCATGAGCAGTGGTAATCTTCTGCTTTTACACCC 938
2y 822 TTCATATCTTGAAGGTCATTCGATCGAATCTGCGCTCTTTCATCA-----GTGT 875
db 939 TATCAGCTCATGCGGAATGAGATGCTTCAAGCCCTGGGGAAGTTGAGAGAGATCAG 998
2y 876 TCCATTGAGATCAGATCCATGAAGCTTACATCGTTTCTAAGCATTAGCTGCTGAAC 935
db 999 TGCACATCAGATCGATCACTCTTTTACATGAGACAGGCTTTGGCTTCTCTGAAC 1058
2y 936 ACCTTGTAACCTGTTACTATATGAGTGTGACAGCGACAATT 979
db 1059 AGTGTCAATCAACCTGTTCTATTTCTTTTGGAGATCACTT 1102

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Search completed: January 30, 2003, 07:08:00
Job time : 916 secs

APPLICANT: Chen, Ruoping
 APPLICANT: Dang, Huong T.
 APPLICANT: Liaw, Chen W.
 APPLICANT: Lin, I-Lin
 TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 FILE REFERENCE: AREN0050
 CURRENT APPLICATION NUMBER: US/10/272,983
 CURRENT FILING DATE: 2002-10-17
 PRIOR APPLICATION NUMBER: US/09/417,044
 PRIOR FILING DATE: 1999-10-12
 PRIOR APPLICATION NUMBER: 60/109,213
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
 PRIOR APPLICATION NUMBER: 60/121,851
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/123,946
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,949
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/136,436
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/136,437
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/136,439
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/136,567
 PRIOR FILING DATE: 1999-05-28
 Remaining Prior Application data removed - See File Wrapper or PAM.
 NUMBER OF SEQ ID NOS: 74
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 35
 LENGTH: 1005
 TYPE: DNA
 ORGANISM: Homo sapiens
 JS-10-272-983-35

Query Match 12.1%; Score 131.2; DB 6; Length 1005;
 Best Local Similarity 49.3%; Pred. No. 5e-27;
 Matches 436; Conservative 0; Mismatches 433; Indels 15; Gaps 3;
 108 GCTGCTTTGGAAATTCGACGTGATGAAATCCCACTCAAGATGACTCTCCCTGTT 167
 25 GCACCTTGCAAAACTGCTGGCAGCAGAGCTGCCCTGGAAGTACTACTCTTCCATT 84
 168 ATTATGCGATTAATCTCTCTGCGGAAATTCAGGCAATGAGATGATATCCACTTAC 227
 85 TTTATGAGATGATGAGTGGTGGAGTCTTGGAATACCATTTGTTTACGGCTAC 144
 228 ATTTCAAAATGAGACCTTGGAGAGCAGCAGCATTTATGTAAGTCACTGACCTGAC 287
 145 ATCTCTCTCTGGAAGACTGGAACGAGATATTTATCTTTAACTCTCTGCTCT 204
 288 GATCTGCTGATATGACCAAGCTCCCTCTCTGATCTACTATGCGAGTGGGAAAC 347
 205 GACTTACCTTTTCTGACACCTCCCATGCTGATTAAGAGATTATGCAAG---AAAC 261
 348 TGGATCTTTGAGATTTCATGATGATTAATCCGCTTCACTTCAACTGAT 407
 262 TGGATATATGAGAGCGTCTCTGATTAAGCAACGATATGCTTCAAGCAACTCTAT 321
 408 AGAGATATCTCTCTCCACCTGTTTCAAGCATTTCCGCTTCACTGATATCAACCA 467
 322 ACCAGCATCTCTCTTCTTCACTTTATATGCAATGATGATTAATTAAGTATCT 381
 468 ATGAGCTCTTTTCTTCACTCAAAACTGATGATGATGATGATGATGATGATGATG 527
 382 TTCGAGAACACCTTCTGCAAAAGAAAGTTGCTATTTATCTCTTGGCAATTTGG 441
 528 ATCATTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 587
 442 GTTTTATGATTAACCTTATGAGTATTAACCACTTCCCTTATTAATCTCTTATTAAC 501

588 AACGATGACCTGCTCTGACCTTACCAAGTTGGATGACTCAATTAATTAAGTGTAC 647
 502 AATGCAACCACTGATTAATGATTTTGGCAAGTTCTGGAGACCCCACTCAACCTGAT 561
 648 AACCTGATTTTGAAGTCACTTCTGCTGCTCCCTCTGGATGATGACCTTGGCAT 707
 562 AGCATGCTCTTACACTGCTTGGGTTCTTATTTCTCTTTTGTGATGTTCTTTTAT 621
 708 ACCAGAT-----ATCCACACTTGAACCAATGATGACCACTGACAGCTGCTTAAG 761
 622 TACAAATGCTGCTCTCTTCAAAAGCAAGAAATGAGAGTGTACTGCTGCTCCCTT 681
 762 CAGAAGCAGAGAGCTTAACCATTTCTGCTACTCTTGCATTTTACATGTTTAAACC 821
 682 GAAAAGCTCTCAACTTGGATCATATGAGAGTGAATCTTCTCTGCTTTTACACCC 741
 822 TTGATATCTTGAAGGATCATTTGGATGAATCTGCTGCTTGAATCA-----GTTGT 875
 742 TATACGTCATGCGGAATGAGATGCTTACGCTGCGGAGTTGAGACAGTATAG 801
 876 TCCATGAGATCAGATCCATGAACTTAACCTGTTCTAGACCATTAAGTCTGTGAC 935
 802 TGCACTGAGTCCGATCACTCCTTTTATGATTTGACACGCTTTGGCTTTCTGAC 861
 936 ACCTTTGGTAACTGTTACTATATGATGATGATGATGATGATGATGATGATGATG 979
 862 AGTGTATCAACCTGCTCTTCTATTTCTTTTGGAGATCACTT 905

RESULT 14
 US-10-264-237-1352
 Sequence 1352, Application US/10264237
 GENERAL INFORMATION:
 APPLICANT: Birse et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: P4131P1
 CURRENT APPLICATION NUMBER: US/10/264,237
 PRIOR FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: PCT/US01/16450
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: US 60/205,515
 PRIOR FILING DATE: 2000-05-19
 NUMBER OF SEQ ID NOS: 2876
 SOFTWARE: PatentIn Ver. 3.1
 SEQ ID NO 1352
 LENGTH: 1436
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-264-237-1352

Query Match 12.1%; Score 131.2; DB 6; Length 1436;
 Best Local Similarity 49.3%; Pred. No. 5.7e-27;
 Matches 436; Conservative 0; Mismatches 433; Indels 15; Gaps 3;
 108 GCTGCTTTGGAAATTCGACGTGATGAAATCCCACTCAAGATGACTCTCCCTGTT 167
 117 GCACCTTGCAAAACTGCTGGCAGCAGAGCTGCCCTGGAAGTACTACTCTTCCATT 176
 168 ATTATGCGATTAATCTCTCTGCGGAAATTCAGGCAATGAGATGATATTCACATTAC 227
 177 TTTATGAGATGATGAGTGGTGGAGTCTTGGAAATACATTTGTTTACGGCTAC 236
 228 ATTTCAAAATGAGACCTTGGAGAGCAGCAGCATTTATGCTGTAACCTGCTGAC 287
 237 ATCTCTCTCTGGAAGACTGGAACAGCAGATATTTATCTTTTAACTCTCTGCTCT 296
 288 GATCGCTGATATGACCAAGCTCCCTCTCTGATTAAGTCACTTATGACAGTGGGAAAC 347
 297 GACTTACCTTTTCTGACACCTCCCATGCTGATTAAGAGATTATGCAATG---AAAC 353
 348 TGGATCTTTGAGATTTCATGATGATTAATCCGCTTCACTTCAATTTCACTGAT 407
 354 TGGATATATGAGAGCGTCTCTGATTAAGCAACGATATGCTTCAATGCAACCTCTAT 413

Db	413	ACCGACGATTCCTCTTCTCAGCTTTATACGACATGATCGATTAATTGAATACCT	4172
Qy	468	ATGAGCTGCTTTCATTCACAAACTGCAATGTCAGTGTAGCTGTGGCTGTGG	52
Db	473	TTCCGAGAAACACTTTCGCAAAAGAAAGATGTCTATTTTAACTCTCTGGCCATGG	5322
Qy	538	ATCATTTCACTGTAGTGTCTTCATTCGATGACCTTCTTGATCATCAACCAAGAGCC	587
Db	533	GTTTATGTAACCTTAGAGTTACGACCAATCTCCCTTAAATCCTGTATTAACCTGAC	5922
Qy	588	AACGATACGCTGTCTCGACCTCACCAAGTTCGATGAATCAATCACTATTAAAGTGTAC	6474
Db	593	AATGCGACCACTGTAAATGATTTGGCAAGTTCTGAGACCCCAACCTACCAACTCATTAC	6522
Qy	648	AACCTGATTTGATCGACAATCTTTGTGCTCCCTTGTGTATGACACATTTGCTAT	7077
Db	653	AGCATGTCTTACACAGTGTGGGGTTCCTTAATCTCTTTTGTGATGTGTCTTTTAT	712
Qy	708	ACCAAGATT-----ATCCACACTCTGACCCATGGAATGCAAACTGACACTGCTTAAG	761
Db	713	TACAGATTTGCTCTCTTCTTAAAGCAAGAAATAGGAGGTGTGCTACTGTGCCCTT	772
Qy	762	CAGAAAGCAGGAAGCTAAACATTTCTCTACTCCCTTGACATTTTAACGATGTTTTAAC	821
Db	773	GAAAGCCTCTCACTGTGTCTATCTATGAGCAGTGTATCTTCTGTGCTTTTAAACCC	8322
Qy	822	TTCCATATCTTGAAGGTCATTCGGATGGAATCTCGCTGCTTCAATCA-----GTGT	8757
Db	833	TATACGCTCATGGGAATGTAGGAGATGCTTCAAGCTCGGGAGTTGGAAGCAGTACAG	892
Qy	876	TTCAATTGAGATCAGATCCATGAAGCTTACATGTTTACAGCAATTAAGTGTCTGAAC	935
Db	893	TGCACTCAGGTGTCAATCACTCCTTTACATGTGACACGGCGCTGTGGCTTCTTGAC	952
Qy	936	ACCTTGTGTAACCTGTACATATATGTGTGTGTAGGAGCAACTT	979
Db	953	AGGTGATCAACCTGTCTTCTAATTTTCTGTGTGGAGATCAACTT	996

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RESULT 11
US-10-270-587-1
; Sequence 1, Application US/10270587
; GENERAL INFORMATION:
; APPLICANT: L1, Y1
; TITLE OF INVENTION: Human G-Protein Coupled Receptor
; FILE REFERENCE: P217C2
; CURRENT APPLICATION NUMBER: US/10/270,587
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 09/908,553
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 08/781,456
; PRIOR FILING DATE: 1997-01-10
; PRIOR APPLICATION NUMBER: US 60/009,902
; PRIOR FILING DATE: 1996-01-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-270-587-1

Query Match      12.4%   Score 134.4, DB 6, Length 1428;
Best Local Similarity 49.5%; Pred. No. 7.le-28;
Matches 438; Conservative 0; Mismatches 431; Indels 15; Gaps 3

QY      108 GCTGCTTTTGGAAATTGCACGTGATGAAGAAACATCCACATCAAGANGCACTACCTCCCTGTT 167
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       116 GCACACTTGCAAAAACCTGCGCTGGCAGCAGAGGCTGCCCTGGAAAAAGTACTACTCTTCATT 175
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      168 ATTATNGCATTAATCTTCCTGTCGGATTTCCAGAGCAATGACATGATGATATCCACTTAC 227

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D6		TTTGGAAATGTGCACTGATGAAAACATCCCATCGAAGATGCATACTCCCTGTATATTAT	120
OY	174	GGCATTATCTTCCTCGTGGGATTTTCAGAGCAAATGACAGTAGATATCACTTACATTTTC	23
D6	121	GGCATTATCTTCCTCGTGGGATTTTCAGAGCAAATGACAGTAGATATCACTTACATTTTC	189
OY	234	AAATGAGACTTGGAAAGCAGACAACATATTAATGCTGAACCTTGACCCTGCAGATCTG	293
D6	181	AAAAATGAACTTGGAAAGCAGACAACATATTAATGCTGAACCTTGACCCTGCAGATCTG	241
OY	294	CTGATCTGACACACCTCCCCCTTCCTGATTCATCTATCTATATGCAATGGCGAAAATCTGATC	353
D6	241	CTGATCTGACACACCTCCCCCTTCCTGATTCATCTATCTATATGCAATGGCGAAAATCTGATC	300
OY	354	TTTTGGAGATTTTCATGTGTAAGTTATCCGCTTGACCTTCATTTCAACTGTATAGGACG	413
D6	301	TTTTGGAGATTTTCATGTGTAAGTTATCCGCTTGACCTTCATTTCAACTGTATAGGACG	360
OY	414	ATCCCTCTTCCCTCACCTGTGTTTCAGCATCTTCCTGCTACTGCTGATCATTCACCCATGAC	477
D6	361	ATCCCTCTTCCCTCACCTGTGTTTCAGCATCTTCCTGCTACTGCTGATCATTCACCCATGAC	424
OY	474	TGCTTTTCCATTCCAACAAATCTGCATATGTCAGTGTGATGCTGTGCTGTGTGGATCATT	533
D6	421	TGCTTTTCCATTCCAACAAATCTGCATATGTCAGTGTGATGCTGTGCTGTGTGGATCATT	480
OY	534	TCACCTGGAGCTGCATTCCTCGATGACATCCTTCTGATGCAATCAACCAACAGAACCAAGA	593
D6	481	TCACCTGGAGCTGCATTCCTCGATGACATCCTTCTGATGCAATCAACCAACAGAACCAAGA	540
OY	594	TCACCTGCTGTGCACTTCACCACTGATTCGAGATGAATCAATCTATTAAGTGTGAACCTG	653
D6	541	TCACCTGCTGTGCACTTCACCACTGATTCGAGATGAATCAATCTATTAAGTGTGAACCTG	600
OY	654	ATTTTGACTGCACTTACTTTCTGCTCTCCCTTGCTGGTGAATGACACTTTGCTATACACG	713
D6	601	ATTTTGACTGCACTTACTTTCTGCTCTCCCTTGCTGGTGAATGACACTTTGCTATACACG	660
OY	714	ATTATTCACACTCTGCACCCANNGACATGCGAATGACAGCTGCCCTTAAGCAGAAAGCAGA	773
D6	661	ATTATTCACACTCTGCACCCANNGACATGCGAATGACAGCTGCCCTTAAGCAGAAAGCAGA	720
OY	774	AGGCTAACATTCCTGCTACTCTCTGTGCAATTTAGATGTTTTTAACTCCCTTCCATATCTTG	833
D6	721	AGGCTAACATTCCTGCTACTCTCTGTGCAATTTAGATGTTTTTAACTCCCTTCCATATCTTG	780
OY	834	AGGGCTATTGGATCGAATCTTCGCTGCTCTTCAATCAATGATTTTCATTGGAATTCAGATC	893
D6	781	AGGGCTATTGGATCGAATCTTCGCTGCTCTTCAATCAATGATTTTCATTGGAATTCAGATC	840
OY	894	CATGAACCTTCAATCGTTTCTTAAGACCTTAATGCTGCTGTGAACACTTTTGGTAACTGTTA	953
D6	841	CATGAACCTTCAATCGTTTCTTAAGACCTTAATGCTGCTGTGAACACTTTTGGTAACTGTTA	900
OY	954	CTATATGTGTGTGTCAGCGCAACAATTCAGACAGCTGTGCTCAACAGTGAATGACAA	1011
D6	901	CTATATGTGTGTGTCAGCGCAACAATTCAGACAGCTGTGCTCAACAGTGAATGACAA	960
OY	1014	GTAAGCGGGAACCTTGAGCAAGCAAAAATTAGTTACTCAACAAACCTTTGA	1067
D6	961	GTAAGCGGGAACCTTGAGCAAGCAAAAATTAGTTACTCAACAAACCTTTGA	1014
RESULT 8			
US-10-296-081-10			
Sequence 10, Application US/10296081			
GENERAL INFORMATION:			
APPLICANT: INCYTE GENOMICS, INC.			
APPLICANT: PATTERSON, Chandra			
APPLICANT: LU, Dzung Anna M.			
APPLICANT: THORNTON, Michael			
APPLICANT: LU, Yan			

db 61 TTGGAAATTCAGCTAGTAAACATCCCACTCAAGATGCACTACCTCCGTTATTAT 120
 174 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGTATTCATTCATTTTC 233
 121 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGTATTCATTCATTTTC 180
 234 AAATAGACCTTGGAGAGAGACCATCTATATGCTGAACCTGGCTGACAGATCTG 293
 181 AAATAGACCTTGGAGAGAGACCATCTATATGCTGAACCTGGCTGACAGATCTG 240
 294 CTGTATCTGACAGACCTCCCTCTCTGATTCATCTATGCGAGTGGGAAAATGATC 353
 241 CTGTATCTGACAGACCTCCCTCTCTGATTCATCTATGCGAGTGGGAAAATGATC 300
 354 TTGGAGATTCATGATGTAAGTTATTCGCTTCAAGCTTCATTTCAACTGTATAGAGC 413
 301 TTGGAGATTCATGATGTAAGTTATTCGCTTCAAGCTTCATTTCAACTGTATAGAGC 360
 414 ATCCCTCTCTCAACCTGTTTCAAGATCTTCGCGTACTGTGTATCATTCACCCATGAGC 473
 361 ATCCCTCTCTCAACCTGTTTCAAGATCTTCGCGTACTGTGTATCATTCACCCATGAGC 420
 474 TGGTTTCCATTCACAAATCTGATGTCAGTGTGATGAGCTGTGCTGTGTATCATTT 533
 421 TGGTTTCCATTCACAAATCTGATGTCAGTGTGATGAGCTGTGCTGTGTATCATTT 480
 534 TCACTGTAGCTGTATTCATTCGATGATGATGATGATGATGATGATGATGATGATG 593
 481 TCACTGTAGCTGTATTCATTCGATGATGATGATGATGATGATGATGATGATGATG 540
 594 TCACTGTAGCTGTATTCATTCGATGATGATGATGATGATGATGATGATGATGATG 653
 541 TCACTGTAGCTGTATTCATTCGATGATGATGATGATGATGATGATGATGATGATG 600
 654 ATTTGATGCTGCACTATCTTCTGCTCCCTGGTGTGATGATGATGATGATGATGATG 713
 601 ATTTGATGCTGCACTATCTTCTGCTCCCTGGTGTGATGATGATGATGATGATGATG 660
 714 ATTTGATGCTGCACTATCTTCTGCTCCCTGGTGTGATGATGATGATGATGATGATG 773
 661 ATTTGATGCTGCACTATCTTCTGCTCCCTGGTGTGATGATGATGATGATGATGATG 720
 774 AGGCTTAACCTTCTGCTACTGCTTGGCATTTTATGATGATGATGATGATGATGATG 833
 721 AGGCTTAACCTTCTGCTACTGCTTGGCATTTTATGATGATGATGATGATGATGATG 780
 834 AGGCTTAACCTTCTGCTACTGCTTGGCATTTTATGATGATGATGATGATGATGATG 893
 781 AGGCTTAACCTTCTGCTACTGCTTGGCATTTTATGATGATGATGATGATGATGATG 840
 894 CATGAGCTTACATCGTTTCTAGACCATAGCTGCTGAAACCTTGTGTAACCTGTTA 953
 841 CATGAGCTTACATCGTTTCTAGACCATAGCTGCTGAAACCTTGTGTAACCTGTTA 900
 954 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1013
 901 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 1014 GTTAAAGGAGAACTTGAAGCAAGCAAAAGAAATTAATTAATTAATTAATTAATTA 1067
 961 GTTAAAGGAGAACTTGAAGCAAGCAAAAGAAATTAATTAATTAATTAATTAATTA 1014

ESUT 5
 IS-10-321-807-27
 Sequence 27, Application US/10321807
 GENERAL INFORMATION:
 APPLICANT: Chen, Rupong
 APPLICANT: Dang, Hong T.
 APPLICANT: Lowitz, Kevin P.
 TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
 FILE REFERENCE: AREN0086

CURRENT APPLICATION NUMBER: US/10/321,807
 PRIOR FILING DATE: 2002-12-16
 PRIOR APPLICATION NUMBER: US/09/714,008
 PRIOR FILING DATE: 2000-11-16
 PRIOR APPLICATION NUMBER: 09/170,496
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: PCT/US99/23938
 PRIOR FILING DATE: 2000-04-20
 PRIOR APPLICATION NUMBER: 60/166,088
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: 60/166,099
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: 60/166,369
 PRIOR FILING DATE: 1999-11-17
 PRIOR APPLICATION NUMBER: 60/171,902
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/171,901
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/171,900
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/181,749
 PRIOR FILING DATE: 2000-02-11
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 133
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 27
 LENGTH: 1014
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-321-807-27

Query Match 93.8%; Score 1014; DB 6; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 5.9e-276;
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ATGATAGACCACTAGTATTTAGCAATGCTTCTGATTTCCCGATTAATGACCTGCT 113
 DB 1 ATGATAGACCACTAGTATTTAGCAATGCTTCTGATTTCCCGATTAATGACCTGCT 60
 QY 114 TTGGAAATTCAGCTAGTAAACATCCCACTCAAGATGCACTACCTCCGTTATTAT 173
 DB 61 TTGGAAATTCAGCTAGTAAACATCCCACTCAAGATGCACTACCTCCGTTATTAT 120
 QY 174 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGTATTCATTCATTTTC 233
 DB 121 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGAGTATTCATTCATTTTC 180
 QY 234 AAATAGACCTTGGAGAGAGACCATCTATATGCTGAACCTGGCTGACAGATCTG 293
 DB 181 AAATAGACCTTGGAGAGAGACCATCTATATGCTGAACCTGGCTGACAGATCTG 240
 QY 294 CTGTATCTGACAGACCTCCCTCTCTGATTCATCTATGCGAGTGGGAAAATGATC 353
 DB 241 CTGTATCTGACAGACCTCCCTCTCTGATTCATCTATGCGAGTGGGAAAATGATC 300
 QY 354 TTGGAGATTCATGATGTAAGTTATTCGCTTCAAGCTTCATTTCAACTGTATAGAGC 413
 DB 301 TTGGAGATTCATGATGTAAGTTATTCGCTTCAAGCTTCATTTCAACTGTATAGAGC 360
 QY 414 ATCCCTCTCTCAACCTGTTTCAAGATCTTCGCGTACTGTGTATCATTCACCCATGAGC 473
 DB 361 ATCCCTCTCTCAACCTGTTTCAAGATCTTCGCGTACTGTGTATCATTCACCCATGAGC 420
 QY 474 TGGTTTCCATTCACAAATCTGATGTCAGTGTGATGAGCTGTGCTGTGTATCATTT 533
 DB 421 TGGTTTCCATTCACAAATCTGATGTCAGTGTGATGAGCTGTGCTGTGTATCATTT 480
 QY 534 TCACTGTAGCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATG 593
 DB 481 TCACTGTAGCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATG 540
 QY 594 TCACTGTAGCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATG 653

Dh	388	GACCTTGGAGAGCAGCAACATCATTATGCTGAACCTGGCCTTGCAAGATCTGCTGATC	447
Qy	301	TGACCAAGCTTCCCTTCTGATTCATATATGCAAGTGGCCGAAAACCTGGATCTTTGGAG	360
Dh	448	TGACCAAGCTTCCCTTCTGATTCATATATGCAAGTGGCCGAAAACCTGGATCTTTGGAG	507
Qy	361	ATTTCATGATGATGATTAATCCGCTCAGCTTCATTTGAAACCTGATATGACGATCCTCT	420
Dh	508	ATTTCATGATGATGATTAATCCGCTCAGCTTCATTTGAAACCTGATATGACGATCCTCT	567
Qy	421	TCTCATCCTGTTTGACGATCTTCCGCTACCTGATGATTCACCAATGAGCTGCTTT	480
Dh	568	TCTCATCCTGTTTGACGATCTTCCGCTACCTGATGATTCACCAATGAGCTGCTTT	627
2y	481	CCATTACAAAACTCGATGTGACAGTTGATGAGCTGTGCTGTGTGTGATCAATTCACGTG	540.
Dh	628	CCATTACAAAACTCGATGTGACAGTTGATGAGCTGTGCTGTGTGTGATCAATTCACGTG	687
2y	541	TAGCGTCAATTCGCAATGACCTTTTGATACATCAACCAACGAGCCAAAGATCAGCT	600
Dh	688	TAGCTGTATTCGCAATGACCTTTTGATACATCAACCAACGAGCCAAAGATCAGCT	747
2y	601	GTCGCACTTCACGAGTTCGAGATGAATCAATATCATTAATGATGATCAACCTGATTTGA	660
Dh	748	GTCGCACTTCACGAGTTCGAGATGAATCAATATCATTAATGATGATCAACCTGATTTGA	807
2y	661	CTGCAACTACTTTCTGCTCCCTCTTGATATGATGACATTTGCTATACCAAGATATCC	720
Dh	808	CTGCAACTACTTTCTGCTCCCTCTTGATATGATGACATTTGCTATACCAAGATATCC	867
2y	721	ACACTCGAACCCATGAGATGCAAACTGACACTGCTTAAGCAGAAAAGCAGAGCTAA	780
Dh	868	ACACTCGAACCCATGAGATGCAAACTGACACTGCTTAAGCAGAAAAGCAGAGCTAA	927
2y	781	CCATTCTGCTACTCCTTGCAATTTATACGATGATTTTAAACCTTCATATCTTGAAGGCTCA	840
Dh	928	CCATTCTGCTACTCCTTGCAATTTATACGATGATTTTAAACCTTCATATCTTGAAGGCTCA	987
2y	841	TTGGGATGCAATCTCGCTGCTTTCATCAGTGTTCATTTAGAGATCAGATCCATGAG	900
Dh	988	TTGGGATGCAATCTCGCTGCTTTCATCAGTGTTCATTTAGAGATCAGATCCATGAG	1047
2y	901	CTTACATCGATTTTACAGCAATTAATCTGCTGCAACACTTTGATACCTGTTACTATATG	960
Dh	1048	CTTACATCGATTTTACAGCAATTAATCTGCTGCAACACTTTGATACCTGTTACTATATG	1107
2y	961	TGGTGTGTCAAGGCAAACTTTTACAGAGGCTGTCTGCTCAACAGTGAATGCAAAAGTAAGC	1020
Dh	1108	TGGTGTGTCAAGGCAAACTTTTACAGAGGCTGTCTGCTCAACAGTGAATGCAAAAGTAAGC	1167
2y	1021	GGAACCTTGAGCAAGCAAAAGAAATTAATTAATCTCAAAACCACTTGAATATATTTCAATTA	1080
Dh	1168	GGAACCTTGAGCAAGCAAAAGAAATTAATTAATCTCAAAACCACTTGAATATATTTCAATTA	1227
2y	1081	C 1081	
Dh	1228	C 1228	

RESULT 2
IS-10-270-144-3
Sequence 3, Application US/10270144
GENERAL INFORMATION:

TITLE OF INVENTION: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: C1.0007500CN
CURRENT APPLICATION NUMBER: US/10/270,144
CURRENT FILING DATE: 2002-10-15
PRIORITY APPLICATION NUMBER: 60/205,196
PRIORITY FILING DATE: 2000-05-18

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9905
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-3

Query Match      100.0%; Score 1081; DB 6; Length 9905;
Best Local Similarity 100.0%; Pred. No. 1,6e-294;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	CATATGCGAAACTGAACCTCTCTGTTTCTTGCAAGATGAAGAGACAACATGAATG	60
Db	8256	CATATGCGAAACTGAACCTCTCTGTTTCTTGCAAGATGAAGAGACAACATGAATG	8315
QY	61	AGCCACTGACCTATTTAGCAAAATGCTTCTGATTTTCCCGATTAATGACCTGTTTGGAA	120
Db	8316	AGCCACTGACCTATTTAGCAAAATGCTTCTGATTTTCCCGATTAATGACCTGTTTGGAA	8375
QY	121	ATTGCACTGAGAAAACATCCCACTCAAGATGACCTACCTCCCTGTTATTTATGCACTTA	180
Db	8376	ATTGCACTGAGAAAACATCCCACTCAAGATGACCTACCTCCCTGTTATTTATGCACTTA	8435
QY	181	TCTTCCTGATGGAAATTTCCAGGGCAATGAGTAGATATCCACTTACATTTTCAAAAATGA	240
Db	8436	TCTTCCTGATGGAAATTTCCAGGGCAATGAGTAGATATCCACTTACATTTTCAAAAATGA	8495
QY	241	GACCTTGGAAAGACAGACCACTATTAATGCTGAACCTGGACCTGACAGATCTGCGTATTC	300
Db	8496	GACCTTGGAAAGACAGACCACTATTAATGCTGAACCTGGACCTGACAGATCTGCGTATTC	8555
QY	301	TGACAGGCTCTCCCTTCTCTGATTCATTAATGCAATGCGAGTGGGAAAATGATCTTTGGAG	360
Db	8556	TGACAGGCTCTCCCTTCTCTGATTCATTAATGCAATGCGAGTGGGAAAATGATCTTTGGAG	8615
QY	361	ATTTCAGTGTGAATTTATCCGCTTCAGCTTCCATTTCACCTGTATAGCAGATCTCT	420
Db	8616	ATTTCAGTGTGAATTTATCCGCTTCAGCTTCCATTTCACCTGTATAGCAGATCTCT	8675
QY	421	TCTCAACCTGTTTACAGCATCTCCGCACTAGTGTGATCATTCACCCCAATGAGCGCTTTT	480
Db	8676	TCTCAACCTGTTTACAGCATCTCCGCACTAGTGTGATCATTCACCCCAATGAGCGCTTTT	8735
QY	481	CCATTCACAAAACTCGATGTGAGTGTAGCTGTGCTGTGTGTGTGATCATTCACCTGG	540
Db	8736	CCATTCACAAAACTCGATGTGAGTGTAGCTGTGCTGTGTGTGTGATCATTCACCTGG	8795
QY	541	TAGCTGCAATTCGAGTACCTTCTTGATCAATCAACCAACAGAGCAACAGATCAGCT	600
Db	8796	TAGCTGCAATTCGAGTACCTTCTTGATCAATCAACCAACAGAGCAACAGATCAGCT	8855
QY	601	GTCCTGACCTCAACGATTTGGATGAATCTAATATCTAATTAATGTGTAACAACCTGAATTTGA	660
Db	8856	GTCCTGACCTCAACGATTTGGATGAATCTAATATCTAATTAATGTGTAACAACCTGAATTTGA	8915
QY	661	CTGCAACTATCTTTCTGCTCTCCCTGGTGTATGTGACACTTTGTGTATACCAACGATTTTC	720
Db	8916	CTGCAACTATCTTTCTGCTCTCCCTGGTGTATGTGACACTTTGTGTATACCAACGATTTTC	8975
QY	721	ACAACCTGACCCATGACCTGCAAACTGACAGCTGCCCTTAAGACAAGAAAGCAAGAGCTTAA	780
Db	8976	ACAACCTGACCCATGACCTGCAAACTGACAGCTGCCCTTAAGACAAGAAAGCAAGAGCTTAA	9035
QY	781	CCATTCTGCTACTCTCTTGCAATTTAGATATGTTTAAACCTTCCATATCTTGAGGGTCA	840
Db	9036	CCATTCTGCTACTCTCTTGCAATTTAGATATGTTTAAACCTTCCATATCTTGAGGGTCA	9095
QY	841	TTTGGATCGAATCTCGCTGCTTTCAATCACTGTGTTCCATTGGAATCAGATCCATGAG	900
Db	9096	TTTGGATCGAATCTCGCTGCTTTCAATCACTGTGTTCCATTGGAATCAGATCCATGAG	9155
QY	901	CTTACATCGTTTCTAACAATTAGCTGCTGTAACAACCTTGGTAAACCTGTATCTATATG	960

/ TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 / TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 / FILE REFERENCE: CL000563
 / CURRENT APPLICATION NUMBER: US/60/205,423
 / CURRENT FILING DATE: 2000-05-19
 / NUMBER OF SEQ ID NOS: 494
 / SOFTWARE: FaastSeq for Windows Version 4.0
 / SEQ ID NO 235
 / LENGTH: 8161
 / TYPE: DNA
 / ORGANISM: HUMAN
 / US-60-205-423-235

Query Match 98.8%; Score 1068.4; DB 64; Length 8161;
 Best Local Similarity 99.8%; Pred. No. 1.9e-295;
 Matches 1080; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

2Y 1 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGATGAAAGAGACAAACATGATG 60
 Db 3368 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGATGAAAGAGACAAACATGATG 3427
 2Y 61 AGCCACTAGACTATTGCAAAATGCTTGAATTTCCCGATTATGACAGCTGTTTGGAA 120
 Db 3428 AGCCACTAGACTATTGCAAAATGCTTGAATTTCCCGATTATGACAGCTGTTTGGAA 3487
 2Y 121 ATTGCACTGATGAAATCATCCACTCAAGATGACACTACCTCCCTGTTATTTATGCGATTA 180
 Db 3488 ATTGCACTGATGAAATCATCCACTCAAGATGACACTACCTCCCTGTTATTTATGCGATTA 3547
 2Y 181 TCTTCCCTCGGGATTTCCAGGCAATGCAAGATGATGATTCACACTTACATTTCAAAATGA 240
 Db 3548 TCTTCCCTCGGGATTTCCAGGCAATGCAAGATGATGATTCACACTTACATTTCAAAATGA 3607
 2Y 241 GACCTTGGAAAGACAGACACATATTAATGCTGAACCTGCTGCAAGATGCTGTATC 300
 Db 3608 GACCTTGGAAAGACAGACACATATTAATGCTGAACCTGCTGCAAGATGCTGTATC 3667
 2Y 301 TGACCAAGCCCTCCCTCTCTGATTCATCTATGCGCATGCGGAAATCGATCTTTGGAG 360
 Db 3668 TGACCAAGCCCTCCCTCTCTGATTCATCTATGCGCATGCGGAAATCGATCTTTGGAG 3727
 2Y 361 ATTTCATGTGATGATTTATCGCTTCACTTCACTTCAACCTGTATAGCGACCTCT 420
 Db 3728 ATTTCATGTGATGATTTATCGCTTCACTTCACTTCAACCTGTATAGCGACCTCT 3787
 2Y 421 TCTCTACCTGTTTCAAGCATCTTCCGCTACTGTTGATCATTTCAACCAATGAGCTGCTTT 480
 Db 3788 TCTCTACCTGTTTCAAGCATCTTCCGCTACTGTTGATCATTTCAACCAATGAGCTGCTTT 3847
 2Y 481 CCATTGCAAAATCGATGTCAGTTGACCTGTGCTGTGTGTGATCATTTCACTGG 540
 Db 3848 CCATTGCAAAATCGATGTCAGTTGACCTGTGCTGTGTGTGATCATTTCACTGG 3907
 2Y 541 TAGCTGTCAATCCGATGACCTTCTGATGATCAATCAACCAAGACCAAGATGACCT 600
 Db 3908 TAGCTGTCAATCCGATGACCTTCTGATGATCAATCAACCAAGACCAAGATGACCT 3967
 2Y 601 GTCTGACCTCAACAGTTGCGATGAATCAATATTAAGTGGTCAACCTGATTTTGA 660
 Db 3968 GTCTGACCTCAACAGTTGCGATGAATCAATATTAAGTGGTCAACCTGATTTTGA 4027
 2Y 661 CTGCAACTATCTTCTGCTCCCTTGGTGTATGATGACATTTGCTATACCAAGATTAATCC 720
 Db 4028 CTGCAACTATCTTCTGCTCCCTTGGTGTATGATGACATTTGCTATACCAAGATTAATCC 4087
 2Y 721 ACACCTGACCAATGAGCTGCAAACTGACAGCTG-CCTTAAAGCAAAAGACGAGGCTA 779
 Db 4088 ACACCTGACCAATGAGCTGCAAACTGACAGCTG-CCTTAAAGCAAAAGACGAGGCTA 4147
 2Y 780 ACCATTTGCTACTCTCTGCAATTTAAGTATGTTTAACTTCCATATCTTGAAGGTC 839
 Db 4148 ACCATTTGCTACTCTCTGCAATTTAAGTATGTTTAACTTCCATATCTTGAAGGTC 4207

QY 840 ATTGGATGAAATCTCGCTGCTTTCATCATAGTTTGTTCATTTAGAAATCATCATGAA 899
 Db 4208 ATTGGATGAAATCTCGCTGCTTTCATCATAGTTTGTTCATTTAGAAATCATCATGAA 4267
 QY 900 GCTTACATGTTTCTAGACCAATAGCTGCTGGAACACCTTGGTAACCTGTACTATAT 959
 Db 4268 GCTTACATGTTTCTAGACCAATAGCTGCTGGAACACCTTGGTAACCTGTACTATAT 4327
 QY 960 GTGTGTGTCAGCGCAACTTTCAAGAGCTGTCTGCTCAACAGTGAATGCAAGTAAGC 1019
 Db 4328 GTGTGTGTCAGCGCAACTTTCAAGAGCTGTCTGCTCAACAGTGAATGCAAGTAAGC 4387
 QY 1020 GGGAACTTGGAGCAAGCAAAATTAATTACTCAAAACCTTGAATAATTTCAATT 1079
 Db 4388 GGGAACTTGGAGCAAGCAAAATTAATTACTCAAAACCTTGAATAATTTCAATT 4447
 QY 1080 AC 1081
 Db 4448 AC 4449

RESULT 15
 US-60-205-423-236
 / Sequence 236, Application US/60205423
 / GENERAL INFORMATION:
 / APPLICANT: Beasley, Ellen
 / TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
 / TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 / FILE REFERENCE: CL000563
 / CURRENT APPLICATION NUMBER: US/60/205,423
 / CURRENT FILING DATE: 2000-05-19
 / NUMBER OF SEQ ID NOS: 494
 / SOFTWARE: FaastSeq for Windows Version 4.0
 / SEQ ID NO 236
 / LENGTH: 8161
 / TYPE: DNA
 / ORGANISM: HUMAN
 / US-60-205-423-236

Query Match 98.8%; Score 1068.4; DB 64; Length 8161;
 Best Local Similarity 99.8%; Pred. No. 1.9e-295;
 Matches 1080; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGATGAAAGAGACAAACATGATG 60
 Db 3368 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGATGAAAGAGACAAACATGATG 3427
 QY 61 AGCCACTAGACTATTGCAAAATGCTTGAATTTCCCGATTATGACAGCTGTTTGGAA 120
 Db 3428 AGCCACTAGACTATTGCAAAATGCTTGAATTTCCCGATTATGACAGCTGTTTGGAA 3487
 QY 121 ATTGCACTGATGAAATCATCCACTCAAGATGACACTACCTCCCTGTTATTTATGCGATTA 180
 Db 3488 ATTGCACTGATGAAATCATCCACTCAAGATGACACTACCTCCCTGTTATTTATGCGATTA 3547
 QY 181 TCTTCCCTCGGGATTTCCAGGCAATGCAAGATGATGATTCACACTTACATTTCAAAATGA 240
 Db 3548 TCTTCCCTCGGGATTTCCAGGCAATGCAAGATGATGATTCACACTTACATTTCAAAATGA 3607
 QY 241 GACCTTGGAAAGACAGACACATATTAATGCTGAACCTGCTGCAAGATGCTGTATC 300
 Db 3608 GACCTTGGAAAGACAGACACATATTAATGCTGAACCTGCTGCAAGATGCTGTATC 3667
 QY 301 TGACCAAGCTCCCTTCTGATTCATCTATGCAAGTGGCGAAAACTGATCTTTGGAG 360
 Db 3668 TGACCAAGCTCCCTTCTGATTCATCTATGCAAGTGGCGAAAACTGATCTTTGGAG 3727
 QY 361 ATTTCATGTGATGATTTATCGCTTCACTTCACTTCAACCTGTATAGCAGATCTCT 420
 Db 3728 ATTTCATGTGATGATTTATCGCTTCACTTCACTTCAACCTGTATAGCAGATCTCT 3787
 QY 421 TCTCTACCTGTTTCAAGCATCTTCCGCTACTGTTGATCATTTCAACCAATGAGCTGCTTT 480

481 CCATTCAAAACTCGATGCGAGTTGACCTGCTGCTGGTGGATCATTCATTCTGG 541
 3848 CCATTCAAAACTCGATGCGAGTTGACCTGCTGCTGGTGGATCATTCATTCTGG 390

; TYPE: DNA
 ; ORGANISM: HUMAN
 US-60-205-423-233


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Oy 541 TAGGTGTCATTCGATGACCTTCTTGATCATCAACCAAGCAAGCAAGATGAGCT 600
Db 781 TAGGTGTCATTCGATGACCTTCTTGATCATCAACCAAGCAAGCAAGATGAGCT 840
Oy 601 GTCTCGACCTGACAGTTCCGATGACCAATCAATCAATCAATCAATCAATCAAT 660
Db 841 GTCTCGACCTGACAGTTCCGATGACCAATCAATCAATCAATCAATCAATCAAT 900
Oy 661 CTGCAACTACTCTTGTGCTCCCTTGTGATGACCACTTGTGATGACCACTTATCC 720
Db 901 CTGCAACTACTCTTGTGCTCCCTTGTGATGACCACTTGTGATGACCACTTATCC 960
Oy 721 ACACTCTGACCCATGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 780
Db 961 ACACTCTGACCCATGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Oy 781 CCAATCTGCTACTCTTGTGATGACCACTTGTGATGACCACTTGTGATGACCACT 840
Db 1021 CCAATCTGCTACTCTTGTGATGACCACTTGTGATGACCACTTGTGATGACCACT 1080
Oy 841 TTGGATGCAATCTGCTGCTGCTTCAATCAATCAATCAATCAATCAATCAATCAAG 900
Db 1081 TTGGATGCAATCTGCTGCTGCTTCAATCAATCAATCAATCAATCAATCAATCAAG 1140
Oy 901 CTACATGCTGTTCTGACACATTAAGTGTGACCACTTGTGATGACCACTTGTGATGAC 960
Db 1141 CTACATGCTGTTCTGACACATTAAGTGTGACCACTTGTGATGACCACTTGTGATGAC 1200
Oy 961 TGGTGGTCAAGGCAACATTTTCAGCAGGCTGTCTGTCAACAGTGAAGTGAAGTGAAG 1020
Db 1201 TGGTGGTCAAGGCAACATTTTCAGCAGGCTGTCTGTCAACAGTGAAGTGAAGTGAAG 1260
Oy 1021 GGAACCTTGAGCAAGCAAAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 1080
Db 1261 GGAACCTTGAGCAAGCAAAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 1320
Oy 1081 C 1081
Db 1321 C 1321

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RESULT 9

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JS-09-785-276A-29927
; Sequence 29927, Application US/09785276A
GENERAL INFORMATION:

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```

APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29927
LENGTH: 1729
TYPE: DNA
ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17
; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-29927

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Query Match 99.9%; Score 1079.4; DB 30; Length 1729;
Best Local Similarity 99.9%; Pred. No. 6,28-229;
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 CATATGCGAAATGGAAGTCTGTTGTTCTTGCAGATGAAGGAGCAACCATGAATG 60
Db 241 CATATGCGAAATGGAAGTCTGTTGTTCTTGCAGATGAAGGAGCAACCATGAATG 300
Oy 61 AGCACTGATGATTTAGCAATGCTTGTGATTTCCCGATTTAGACAGCTGTTTGA 120
Db 301 AGCACTGATGATTTAGCAATGCTTGTGATTTCCCGATTTAGACAGCTGTTTGA 360
Oy 121 ATTGCACTGATGAAGCAATCCCACTCAAGATGACCTGCTGTTATTTATGSCATTA 180
Db 361 ATTGCACTGATGAAGCAATCCCACTCAAGATGACCTGCTGTTATTTATGSCATTA 420
Oy 181 TCTTCCTGAGGATTTCCAGCAATGCAATGATGATATCCACTTAATTTTCAAAATGA 240
Db 421 TCTTCCTGAGGATTTCCAGCAATGCAATGATGATATCCACTTAATTTTCAAAATGA 480
Oy 241 GACCTTGAAGAGAGCAACATCAATTAATGCTGAACCTGCGCTGCAAGATGCTGATC 300
Db 481 GACCTTGAAGAGAGCAACATCAATTAATGCTGAACCTGCGCTGCAAGATGCTGATC 540
Oy 301 TGACAGGCTCCCTCTGATTAATCACTATGCAATGAGGAGAAACATGATCTTTGAG 360
Db 541 TGACAGGCTCCCTCTGATTAATCACTATGCAATGAGGAGAAACATGATCTTTGAG 600
Oy 361 ATTTCATGATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGATGAGCAATCTCT 420
Db 601 ATTTCATGATGATTTATCCGCTTCAAGCTTCAATTTCAACCTGATGAGCAATCTCT 660
Oy 421 TCTTCACCTGTTTCAAGATCTTCCGCTAATGATGATCAATTCACCAATGAGCTGTTT 480
Db 661 TCTTCACCTGTTTCAAGATCTTCCGCTAATGATGATCAATTCACCAATGAGCTGTTT 720
Oy 481 CCATTCAAAACCTGATGAGCAATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 721 CCATTCAAAACCTGATGAGCAATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Oy 541 TAGGTGTCATTCGATGACCTTCTTGATCATCAACCAAGCAAGCAAGATGAGCT 600
Db 781 TAGGTGTCATTCGATGACCTTCTTGATCATCAACCAAGCAAGCAAGATGAGCT 840
Oy 601 GTCTCGACCTGACAGTTCCGATGACCAATCAATCAATCAATCAATCAATCAATCAAT 660
Db 841 GTCTCGACCTGACAGTTCCGATGACCAATCAATCAATCAATCAATCAATCAATCAAT 900
Oy 661 CTGCAACTACTCTTGTGCTCCCTTGTGATGACCACTTGTGATGACCACTTATCC 720
Db 901 CTGCAACTACTCTTGTGCTCCCTTGTGATGACCACTTGTGATGACCACTTATCC 960
Oy 721 ACACTCTGACCCATGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 780
Db 961 ACACTCTGACCCATGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Oy 781 CCAATCTGCTACTCTTGTGATGACCACTTGTGATGACCACTTGTGATGACCACTTATCC 840
Db 1021 CCAATCTGCTACTCTTGTGATGACCACTTGTGATGACCACTTGTGATGACCACTTATCC 1080
Oy 841 TTGGATGCAATCTGCTGCTGCTTCAATCAATCAATCAATCAATCAATCAATCAAG 900
Db 1081 TTGGATGCAATCTGCTGCTGCTTCAATCAATCAATCAATCAATCAATCAATCAAG 1140
Oy 901 CTACATGCTGTTCTGACACATTAAGTGTGACCACTTGTGATGACCACTTGTGATGAC 960
Db 1141 CTACATGCTGTTCTGACACATTAAGTGTGACCACTTGTGATGACCACTTGTGATGAC 1200

```

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APPLICANT: White, David
TITLE OF INVENTION: Novel Seven-Transmembrane
FILE REFERENCE: 5800-67
CURRENT APPLICATION NUMBER: US/09/475,790
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1729
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (294)...(1307)
US-09-475-790-2
Query Match 99.9%; Score 1079.4; DB 18; Length 1729;
Best Local Similarity 99.9%; Pred. No. 6.2e-299;
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGAGACACCATGATG 60
Db 241 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGAGACACCATGATG 300
Qy 61 AGCCACTAGACTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 120
Db 301 AGCCACTAGACTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 360
Qy 121 ATTGCACTGATGAAAACATCCCACTCAAGATGACATACCTCCCTGTTATTTATGACATTA 180
Db 361 ATTGCACTGATGAAAACATCCCACTCAAGATGACATACCTCCCTGTTATTTATGACATTA 420
Qy 181 TCTTCCTCTGTGGGATTTCCAGGCAATGAGTAGTAGATATCCACTTACATTTTCAAAATGA 240
Db 421 TCTTCCTCTGTGGGATTTCCAGGCAATGAGTAGTAGATATCCACTTACATTTTCAAAATGA 480
Qy 241 GACCTTGAAGAGAGAGACATCATATGCTGTAACCTGGCCGACAGATCTGCTATG 300
Db 481 GACCTTGAAGAGAGAGACATCATATGCTGTAACCTGGCCGACAGATCTGCTATG 540
Qy 301 TGACCAAGCTCCCTCTCTGATTCATCTATGCGAGTGGCAAAATGATCTTTGGAG 360
Db 541 TGACCAAGCTCCCTCTCTGATTCATCTATGCGAGTGGCAAAATGATCTTTGGAG 600
Qy 361 ATTTCATGATGATGATTTATCGGCTTCACTTCCATTTCAACCTGTATAGACATCTCT 420
Db 601 ATTTCATGATGATGATTTATCGGCTTCACTTCCATTTCAACCTGTATAGACATCTCT 660
Qy 421 TCCGCACTGTTTGAAGCATCTTCCGCTACTGTGATCATTCACCAATGAGCTGCTTT 480
Db 661 TCCGCACTGTTTGAAGCATCTTCCGCTACTGTGATCATTCACCAATGAGCTGCTTT 720
Qy 481 CCATTGCAAAACATGAGTGCAGTGTGAGCTGTGCTGTGTGATCATTTTACTG 540
Db 721 CCATTGCAAAACATGAGTGCAGTGTGAGCTGTGCTGTGTGATCATTTTACTG 780
Qy 541 TAGCTGTCAATTCAGATGCTTCTTGTATCATCATCAACGAGCAAGATGAGCT 600
Db 781 TAGCTGTCAATTCAGATGCTTCTTGTATCATCATCAACGAGCAAGATGAGCT 840
Qy 601 GTCTGCACTTCAAGTGGATGATGAACTCAATTAATTAAGTGTATCAACTGATTTTGA 660
Db 841 GTCTGCACTTCAAGTGGATGATGAACTCAATTAATTAAGTGTATCAACTGATTTTGA 900
Qy 661 CTGCAATCTACTTCTGCTCCCTCTGTGTGATGATGAGCACTTTGCTATTCACATATATCC 720
Db 901 CTGCAATCTACTTCTGCTCCCTCTGTGTGATGATGAGCACTTTGCTATTCACATATATCC 960
Qy 721 ACACTGACCCCAATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAAGAGGCTAA 780
Db 961 ACACTGACCCCAATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAAGAGGCTAA 1020

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Qy 781 CCATCTGCTACTCCCTGGCATTTTAAGTATGTTTAAACCTTCATATCTGAGGCTCA 840
Db 1021 CCATCTGCTACTCCCTGGCATTTTAAGTATGTTTAAACCTTCATATCTGAGGCTCA 1080
Qy 841 TTGGATGCAATCTGCGCTCTTCAATCATGATGTTTCAATGAGATGATCATGAG 900
Db 1081 TTGGATGCAATCTGCGCTCTTCAATCATGATGTTTCAATGAGATGATCATGAG 1140
Qy 901 CTTCATGCTTTCTAGACCATTAAGCTGCTCTGAGACACCTTTGGTAACTGTATATATG 960
Db 1141 CTTCATGCTTTCTAGACCATTAAGCTGCTCTGAGACACCTTTGGTAACTGTATATATG 1200
Qy 961 TGGTGTGAGGAGCAACTTTCAGAGGCTGTCTGTCTCAACAGTGAAGTGAAGCG 1020
Db 1201 TGGTGTGAGGAGCAACTTTCAGAGGCTGTCTGTCTCAACAGTGAAGTGAAGCG 1260
Qy 1021 GGAACCTTGAGCAAGCAAAATTAAGTACTCAACACCTTGAATATTTGATTA 1080
Db 1261 GGAACCTTGAGCAAGCAAAATTAAGTACTCAACACCTTGAATATTTGATTA 1320
Qy 1081 C 1081
Db 1321 C 1321

```

```

RESULT 7
US-09-785-276A-24015
Sequence 24015, Application US/09785276A
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-0078
CURRENT APPLICATION NUMBER: US/09/785,276A
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24015
LENGTH: 1729
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17
OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-24015

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Query Match 99.9%; Score 1079.4; DB 30; Length 1729;
Best Local Similarity 99.9%; Pred. No. 6.2e-299;
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGAGACACCATGATG 60
Db 241 CATATGGCAAGTGAAGTCTCTGTTTCTTGGCAAGATGAAAGAGACACCATGATG 300
Qy 61 AGCCACTAGACTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 120
Db 301 AGCCACTAGACTATTAGCAATGCTTGATTTCCCGATTATGAGCTGTTTGA 360

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22 1068.4 98.8 11303 64 US-60-200-364-46 Sequence 46, Appl
23 1068.4 98.8 11303 64 US-60-200-364-47 Sequence 47, Appl
24 1068.4 98.8 11303 64 US-60-200-364-48 Sequence 48, Appl
25 1068.4 98.8 11303 64 US-60-200-364-49 Sequence 49, Appl
26 1068.4 98.8 11303 64 US-60-200-364-50 Sequence 50, Appl
27 1068.4 98.8 11303 64 US-60-200-364-51 Sequence 51, Appl
28 1068.4 98.8 11303 64 US-60-200-364-52 Sequence 52, Appl
29 1068.4 98.8 11303 64 US-60-200-364-53 Sequence 53, Appl
30 1068.4 98.8 11303 64 US-60-200-364-54 Sequence 54, Appl
31 1058 97.9 1068 75 US-60-311-340-1 Sequence 1, Appl
32 1014 93.8 1014 24 US-09-634-656-1 Sequence 1, Appl
33 1014 93.8 1014 28 US-09-714-008A-27 Sequence 27, Appl
34 1014 93.8 1014 33 US-09-885-453-2 Sequence 2, Appl
35 1014 93.8 1014 35 US-09-943-798-3 Sequence 3, Appl
36 1014 93.8 1014 37 US-09-955-543-27 Sequence 13, Appl
37 1014 93.8 1014 39 US-10-079-384-13 Sequence 27, Appl
38 1014 93.8 1014 39 US-10-096-511-27 Sequence 27, Appl
39 1013.4 93.7 1015 65 US-60-212-655-973 Sequence 973, Appl
40 1012.4 93.7 1014 22 US-09-569-137-1 Sequence 1, Appl
41 1012.4 93.7 1014 37 US-09-988-922-33 Sequence 33, Appl
42 1012.4 93.7 1014 38 US-10-023-775B-1 Sequence 1, Appl
43 1012.4 93.7 1014 40 US-10-125-748-33 Sequence 33, Appl
44 1012.4 93.7 1014 64 US-60-207-556-2 Sequence 2, Appl
45 1012.4 93.7 1015 66 US-60-229-515-1722 Sequence 1722, Ap

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ALIGNMENTS

RESULT 1

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US-10-010-568-1
: Sequence 1, Application US/10010568
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBM23, EXPRESSED HI
: TITLE OF INVENTION: KIDNEY
: FILE REFERENCE: D0077 NP
: CURRENT APPLICATION NUMBER: US/10/010,568
: CURRENT FILING DATE: 2001-12-07
: PRIOR APPLICATION NUMBER: US 60/251,926
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 60/269,795
: PRIOR FILING DATE: 2001-02-14
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 1081
: TYPE: DNA
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (54)..(1064)
US-10-010-568-1

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Query Match 100.0%; Score 1081; DB 38; Length 1081;
Best Local Similarity 100.0%; Pred. No. 1.7e-299;
Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CATATTGCCAACTGGAAGTCTCTGTTGTTTCTGCAAGATGGAAGAGACAACCATGAATG 60
DB 1 CATATTGCCAACTGGAAGTCTCTGTTGTTTCTGCAAGATGGAAGAGACAACCATGAATG 60
QY 61 AGCAGTAGAGTATTTAGCAATGCTTGTGATTTCCCGATTATGACGCTGTTTGGAA 120
DB 61 AGCAGTAGAGTATTTAGCAATGCTTGTGATTTCCCGATTATGACGCTGTTTGGAA 120
QY 121 ATTGACGTGATGAAATCCCACTCAAGATGACCTACCTCCGTTATTTATGACATTA 180
DB 121 ATTGACGTGATGAAATCCCACTCAAGATGACCTACCTCCGTTATTTATGACATTA 180
QY 181 TCTTCTCGTGGGATTTCCAGGCAATGAGTAGATATCCACTTACATTTTCAAAATGA 240
DB 181 TCTTCTCGTGGGATTTCCAGGCAATGAGTAGATATCCACTTACATTTTCAAAATGA 240

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QY 241 GACCTTGAAGAGACGACCATCATATATGCTGAACCTGGCTGCAAGATCTGCTATTC 300
DB 241 GACCTTGAAGAGACGACCATCATATATGCTGAACCTGGCTGCAAGATCTGCTATTC 300
QY 301 TGACAGGCTCCCTTCCTGATTTACTATCTATGCAAGTGGGAAATCTGATCTTTGGAG 360
DB 301 TGACAGGCTCCCTTCCTGATTTACTATCTATGCAAGTGGGAAATCTGATCTTTGGAG 360
QY 361 ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGAGCATCCCT 420
DB 361 ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGAGCATCCCT 420
QY 421 TCTTCACCTGTTTACAGATCTTCGCTACTGTGTGATCATTTCAACCAATGAGCTGCTTT 480
DB 421 TCTTCACCTGTTTACAGATCTTCGCTACTGTGTGATCATTTCAACCAATGAGCTGCTTT 480
QY 481 CCATTGCAAAATCCGATGTCAGTTGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 481 CCATTGCAAAATCCGATGTCAGTTGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 541 TAGCTGATTTCCGATGTCAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 541 TAGCTGATTTCCGATGTCAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 GTCTGACCTGACAGTTCGATGTAATCTAATATTAAGTGTACCACTGATTTTGA 660
DB 601 GTCTGACCTGACAGTTCGATGTAATCTAATATTAAGTGTACCACTGATTTTGA 660
QY 661 CTGCACTATTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 CTGCACTATTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 ACACCTGACCCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780
DB 721 ACACCTGACCCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780
QY 781 CCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 CCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 TTGCGATGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 TTGCGATGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 CTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TGGTGTGACGCAAACTTTGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 TGGTGTGACGCAAACTTTGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GGAACCTTGAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
DB 1021 GGAACCTTGAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
QY 1081 C 1081
DB 1081 C 1081

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RESULT 2

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US-60-251-926-1
: Sequence 1, Application US/60251926
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBM23, EXPRESSED I
: TITLE OF INVENTION: KIDNEY
: FILE REFERENCE: D0077 PSP
: CURRENT APPLICATION NUMBER: US/60/251,926
: CURRENT FILING DATE: 2000-12-07
: NUMBER OF SEQ ID NOS: 35

```

CURRENT APPLICATION NUMBER: US/09/962,832
 CURRENT FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/60/235,077
 PRIOR FILING DATE: 2000-09-25
 PRIOR APPLICATION NUMBER: US/60/235,280
 PRIOR FILING DATE: 2000-09-25
 NUMBER OF SEQ ID NOS: 259
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 218
 LENGTH: 2051
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-962-832-218

Query Match 7.7%; Score 82.8; DB 10; Length 2051;
 Best Local Similarity 52.0%; Pred. No. 2e-14; Mismatches 172; Indels 0; Gaps 0;

Matches 186; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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2y 183 TTCTCGTGGGATTTCCAGGCAATGCAATGATATCCACTTACATTTTCAAAATGAGA 242
2b 172 TTTATCTTTGGGCTTGGGCAATGGCTTGCCTGTGGATTTCTGTTCCACTCAAG 231
2y 243 CTTGGAAGAGCAGCACCATCATATATGCTGAACCTGGCTGCAAGATCTGCTATCTG 302
2b 232 TCCGGAATCCAGCCGGAATTTCTGTTCAACTGCGAGTAGCTGACTTCTACTGATC 291
2y 303 ACCAGCTCCCTCCCTGATCTACTATAGCCAGTGGCAAACTGATCTTGGAGAT 362
2b 292 ATCTGCTGCGCTTGGATGAGTACTATATGCGGCTTCACTGGAACCTTGGGGAC 351
2y 363 TTCAATGTAGTATTCAGCTTCCGCTACCTGATCTTCACTTCACTGATAGCAGATCTTC 422
2b 352 ATCCCTTGGCGGCTGCTGCTTCTTCACTGTTGGCATGAACCCGAGGAGCATCATCTTC 411
2y 423 CTGACCTGTTTCAAGATCTTCCGCTACTGATGATCATTTACCCCATGAGCTGCTTTTC 482
2b 412 CTCACGGTGGTGGGATGACAGGATATTCGGGTGTCATCCCAACGACCTGAAC 471
2y 483 ATTCAAAACTCGATGTGAGTGTGAGCTGTGCTGTGATGATCATTTCACTGG 540
2b 472 AAGATCTCAATGAGAGCAGCAGCATCATCTTGCCTTCTGTGGGGCATCATGTTG 529

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RESULT 15
 JS-09-944-807-20

Sequence 20, Application US/09944807
 Patent No. US2002011949A1

GENERAL INFORMATION:

APPLICANT: Boehringer Ingelheim Pharma KG
 TITLE OF INVENTION: Method for identifying substances which positively
 TITLE OF INVENTION: influence inflammatory conditions of chronic
 TITLE OF INVENTION: inflammatory airway diseases
 FILE REFERENCE: 082.00n
 CURRENT APPLICATION NUMBER: US/09/944,807
 CURRENT FILING DATE: 2001-08-31
 PRIOR APPLICATION NUMBER: UK 0021484.1
 PRIOR FILING DATE: 2000-09-01
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 20

LENGTH: 2051
 TYPE: DNA
 ORGANISM: Homo sapiens
 JS-09-944-807-20

Query Match 7.7%; Score 82.8; DB 10; Length 2051;
 Best Local Similarity 52.0%; Pred. No. 2e-14; Mismatches 172; Indels 0; Gaps 0;

Matches 186; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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2y 183 TTCTCGTGGGATTTCCAGGCAATGCAATGATATCCACTTACATTTTCAAAATGAGA 242
2b 172 TTTATCTTTGGGCTTGGGCAATGGCTTGCCTGTGGATTTCTGTTCCACTCAAG 231

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Qy 243 CTTGGAAGAGCAGCACCATCATATATGCTGAACCTGGCTGCAAGATCTGCTATCTG 302
Db 232 TCCGGAATCCAGCCGGAATTTCTGTTCAACTGCGAGTAGCTGACTTCTACTGATC 291
Qy 303 ACCAGCTCCCTCCCTGATCTACTATAGCCAGTGGCAAACTGATCTTGGAGAT 362
Db 292 ATCTGCTGCGCTTGGATGAGTACTATATGCGGCTTCACTGGAACCTTGGGGAC 351
Qy 363 TTCAATGTAGTATTCAGCTTCCGCTACCTGATCTTCACTTCACTGATAGCAGATCTTC 422
Db 352 ATCCCTTGGCGGCTGCTGCTTCTTCACTGTTGGCATGAACCCGAGGAGCATCATCTTC 411
Qy 423 CTGACCTGTTTCAAGATCTTCCGCTACTGATGATCATTTCACTGATAGCAGATCTTC 482
Db 412 CTCACGGTGGTGGGATGACAGGATATTCGGGTGTCATCCCAACGACCTGAAC 471
Qy 483 ATTCAAAACTCGATGTGAGTGTGAGCTGTGCTGTGATGATCATTTCACTGG 540
Db 472 AAGATCTCAATGAGAGCAGCAGCATCATCTTGCCTTCTGTGGGGCATCATGTTG 529

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Search completed: January 30, 2003, 06:50:14
 Job time : 87 secs

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; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 799
; CURRENT APPLICATION NUMBER: US/09/728,952
; CURRENT FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: pf_genes Version 2.0
; SEQ ID NO 26
; LENGTH: 1700
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1272)
; NAME/KEY: misc_feature
; LOCATION: (1)..(1700)
; OTHER INFORMATION: n = a,t,c or g
US-09-728-952-26

Query Match      8.7%; Score 93.6; DB 10; Length 1700;
Best Local Similarity 52.3%; Pred. No. 1,1e-17;
Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

2Y 145 TCAGATGACCTACCTCCCTGTTATTTATGCAATTTCTCTGCGGATTTCCAGGCA 204
    |||||
Db 338 TCAGAGAGAAATTTTCCCAATGTATATCGATAATATTTTCTGGGAGCTTGGGAA 397

2Y 205 ATGCAGATGATATTCACCTACATTTTCAAAATGAGACCTTGAAGACGACCAATCA 264
    |||||
Db 398 ATGGGTTTCCATATATATGTTTCTCGACGCTTATTAAGAGTCCATCTGTAAACGTT 457

2Y 265 TTATGTGAACCTGCGCTGACAGATCTGTATCTGACCAAGCTCCCTCTCTGATTC 324
    |||||
Db 458 TCATGTAAATCTGGCATTTTCAGATCTCCGTTCATAGACGCTTCCCTTACGGGCTG 517

2Y 325 ACTACTATGCGCAATGCGGAAATCTGATCTTGGAGATTGATGTAAATTCGCT 384
    |||||
Db 518 ACTATTAATCTTAAGAGGCTCCCAATTTGGAACCTGCGCTGACGATTTATGCTT 577

2Y 385 TCAGTTCATTTCAACCTGTATAGAGCAATCCCTTCCCTGACCTGTTTCAGATTTCC 444
    |||||
Db 578 ATTCCTTGATATGTCATGATGACAGAGATTTATTTCTTCAACGCTGTGATGTGTC 637

2Y 445 GCATCTGTGTATCATTTCAACCAATGAGCTGCTTTCCATTCACAAAACCTGATGTGAG 504
    |||||
Db 638 GTTCTCTGGCAATGTTCAACCCCTTTGGGCTTCTGCAATGACACGATCAGAGAGTCT 697

2Y 505 TTGTAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
    |||||
Db 698 GATCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 733

RESULT 11
JS-09-788-133-1
; Sequence 1, Application US/09788133
; Patent No. US20020052001A1
; GENERAL INFORMATION:
; APPLICANT: GILAXO GROUP LTD
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P79011
; CURRENT APPLICATION NUMBER: US/09/788,133
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1020)
JS-09-788-133-1

Query Match      8.4%; Score 90.8; DB 10; Length 1020;
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Best Local Similarity 47.7%; Pred. No. 5.9e-17;
Matches 309; Conservative 0; Mismatches 327; Indels 12; Gaps 1;

QY 183 TTCCCTGGGATTTTCCAGGCAATGCACTAGTATATCCACTTCAATTTCAAAATAGA 242
    |||||
Db 124 TTATATCTGGCTTTAGTTGGCAATACCTGGCTCTGTGGCTTTTCATCCGAGACCAAG 183

QY 243 CTTTGAAGACAGCAACCATATATATGCTGAACCTGGCTGACAGATCTGCTATCTG 302
    |||||
Db 184 TCCGGACCCCGGCAACGATGTTCTGATGATCTGCGCGGCGCATTTGCGCGTG 243

QY 303 ACCAGCTCCCTTCTGTATCTACTATGCAAGGCGAAATCTGATCTTTGGAGAT 362
    |||||
Db 244 CTGGTCTGCGCAACCCGCTGTGTATCAACATTTCTGGAAACATGCGCATTTGGGAA 303

QY 363 TTCAATGTAAATTTATCCGTTTCACTTCAATTTCAACCTGTATAGAGATCTCTTC 422
    |||||
Db 304 ATGCATGCGCTTACCGGCTTCTCTTCAACCAATGATGCGGACATTAATCTTC 363

QY 423 CTCACCTGTTTCAACATCTTCCGCTACTGTGTATCAATTCACCAATGAGCTTTTCC 482
    |||||
Db 364 CTCACCTGATACAGCGCGACCGTTTCTGTGCAATGTGACCCGCTCAAGTCCCTCAAG 423

QY 483 ATTCAAAACTCGATGTGCAATTTGAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGT 542
    |||||
Db 424 CTCGCAAGGCTCTTACGACACCTGGCGTGTCTTCTGTGTGTGTGTGTGTGTGTGTGT 483

QY 543 GCTGTATCTGATGACCTTTTATATCAATCAACCAAGACCAACAGATCAGCTGT 602
    |||||
Db 484 GCAATGCGCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 543

QY 603 CTGACCTCAACCAATGGAATGAATCAATTAATTAAGTGTACACCTGATTTTGAAT 662
    |||||
Db 544 CTGACCTGTACCGGAAAGGCTCCACCATGCTC-----CTGTGTGCTGTG 591

QY 663 GCAATCACTTCTGCTCTCCCTTGTGTATGTGACACTTGTCTATACCATTAATCCAC 722
    |||||
Db 592 GCAATGCGCTTCACTTCCGTTATCATCACAGGTCAACCTGTCTGTGTGTGTGTGTGTGT 651

QY 723 ACTGTACCAATGACGTGCAACTGACAGCTGCTTGAAGCAAGAAAGCAAGAGCTAAC 782
    |||||
Db 652 AGCTGTGGGCGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 711

QY 783 ATTCGTACTCCCTGATTTTATGTAATTTTATACCTTCCATATC 830
    |||||
Db 712 GCCATGATGCTGCGCATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759

RESULT 12
US-09-880-107-2143
; Sequence 2143, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2143
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797
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APPLICANT: Pfizer Inc
TITLE OF INVENTION: No. US20010039037A1el Polypeptide
FILE REFERENCE: PC10914ADAM
CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 993
TYPE: DNA
ORGANISM: Homo sapiens
US-09-826-791-1

Query Match
Best Local Similarity 52.3%; Score 93.6; DB 10; Length 993;
Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 145 TCAAGATGCACTACCTCCCTGTTATTATGCAATTATCTCTCGTGGATTTCAGGCA 204
Db 59 TCAAGAGAGATTTTCCCAATTGTAATCTGATTAATTTTCTGGGAGCTTGGGAA 118
Qy 205 ATGCACTAGTATATCCATTATCAATTTTCAAAATGAGACCTTGGAAAGAGACCATCA 264
Db 119 ATGGGTTCATATATGTTTCTGACGCTTATAGAAATCCACATCTGTGAACCTTT 178
Qy 265 TTATGCTGAACCTGCGCTGACAGATCTGCTGTATCTGACACGCTCCCTCTGATTC 324
Db 179 TCATGCTAAATCTGGCCATTTCAGATCTCTGTTCAATAGACGCTTCCCTTACGGCTG 238
Qy 325 ACTAGTATGCACTACCTCCCTGTTATTATGCAATTATCTCTGATTTATTCGCT 384
Db 239 ACTATATCTTGAAGGCTCCCAATTGATATTTGAGACCTGCGCTGAGATTAATGCTT 298
Qy 385 TCAGCTTCATTTCAACCTGTATAGAGACATCTCTTCCCACTGTTTCAGATCTTCC 444
Db 299 ATTCCTGTATGTCACATGTAACAGATATTTATTTCCGACCGCTGAGTGTGTGC 358
Qy 445 GCTACTGTGTGATCATTCACCAATGAGCTGCTTTTCAATTCACAAACTCGATGTGAG 504
Db 359 GTTTCCTGGCAATGTTGACCCCTTCCGCTTGTGATGTACACACATCAGAGATGCT 418
Qy 505 TTGTAGCTGTCTGCTGT 540
Db 419 GGATCTCTGTGGATCATATGATGATCTTATCATG 454

RESULT 6
US-09-826-478-1

Sequence 1, Application US/09828478
Patent No. US2002015528A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human Cx36.2-Like GPCR
FILE REFERENCE: 04974.00458
CURRENT APPLICATION NUMBER: US/09/828,478
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo sapiens
US-09-826-478-1

Query Match
Best Local Similarity 52.3%; Score 93.6; DB 9; Length 1041;
Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 145 TCAAGATGCACTACCTCCCTGTTATTATGCAATTATCTCTCGTGGATTTCAGGCA 204
Db 107 TCAAGAGAGATTTTCCCAATTGTAATCTGATTAATTTTCTGGGAGCTTGGGAA 166
Qy 205 ATGCACTAGTATATCCATTATCAATTTTCAAAATGAGACCTTGGAAAGAGACCATCA 264
Db 167 ATGGGTTCATATATGTTTCTGACGCTTATAGAAATCCACATCTGTGAACCTTT 226
Qy 265 TTATGCTGAACCTGCGCTGACAGATCTGCTGTATCTGACACGCTCCCTCTGATTC 324
Db 227 TCATGCTAAATCTGGCCATTTCAGATCTCTGTTCAATAGACGCTTCCCTTACGGCTG 286
Qy 325 ACTAGTATGCACTACCTCCCTGTTATTATGCAATTATCTCTGATTTATTCGCT 384
Db 287 ACTATATCTTGAAGGCTCCCAATTGATATTTGAGACCTGCGCTGAGATTAATGCTT 346
Qy 385 TCAGCTTCATTTCAACCTGTATAGAGACATCTCTTCCCACTGTTTACGATCTTCC 444
Db 347 ATTCCTGTATGTCACATGTAACAGATATTTATTTCTGACCGCTGAGTGTGTGC 406
Qy 445 GCTACTGTGTGATCATTCACCAATGAGCTGCTTTTCAATTCACAAACTCGATGTGAG 504
Db 407 GTTTCCTGGCAATGTTGACCCCTTCCGCTTGTGATGTACACATCAGAGATGCTCT 466
Qy 505 TTGTAGCTGTCTGCTGT 540
Db 467 GGATCTCTGTGGATCATATGATGATCTTATCATG 502

RESULT 7
US-09-826-791-5

Sequence 5, Application US/09826791
Patent No. US20010039037A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
TITLE OF INVENTION: No. US20010039037A1el Polypeptide
FILE REFERENCE: PC10914ADAM
CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (1041)
US-09-826-791-5

Query Match
Best Local Similarity 52.3%; Score 93.6; DB 10; Length 1041;
Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

Qy 145 TCAAGATGCACTACCTCCCTGTTATTATGCAATTATCTCTCGTGGATTTCAGGCA 204
Db 107 TCAAGAGAGATTTTCCCAATTGTAATCTGATTAATTTTCTGGGAGCTTGGGAA 166
Qy 205 ATGCACTAGTATATCCATTATCAATTTTCAAAATGAGACCTTGGAAAGAGACCATCA 264
Db 167 ATGGGTTCATATATGTTTCTGACGCTTATAGAAATCCACATCTGTGAACCTTT 226
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Db 227 TCATGCTAAATCTGGCCATTTCAGATCTCTGTTCAATAGACGCTTCCCTTACGGCTG 286

475 TCCTACACCTTACATGGAACAACCTGGGTTCAGGGAGGCCCTTGACAGGTCATTT 534
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 444 CGCTACTGTGTATCATTCACCAATGAGCTGCTTTTCCATTCAAAAATCTCGATGTGCA 503
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 504 GTTGTAGCTGTGCTGTGTGTGTGATTCATTTCACTGTAGCTGTC 548
 655 GGCCTCTCTTGGCAATCTGCTCTGATTTTCTGTGTACCATTC 699
 RESULT 15
 JS-08-472-840-60
 Sequence 60, Application US/08472840
 Patent No. 5763575
 GENERAL INFORMATION:
 APPLICANT: SUNDELIN, JOHAN
 APPLICANT: SCARBOROUGH, ROBERT M.
 TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
 TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,840
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/390,301
 FILING DATE: 25-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: ADLER, REID G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 2803-0006.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2732 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 73..1269
 JS-08-472-840-60

Query-Match 9.0%; Score 97.8; DB 1; Length 2732;
 Best Local Similarity 52.6%; Pred. No. 6e-20;
 Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

144 CTGAGATGCACTTCCCTGTTATTTATGCAATATCTTCTGTTGGATTTCCAGGC 203
 295 CTGACCAAGGCTCTTCTCGGTCTGCTACATTAATGTTGTGATGTTGCTTCCAGT 354
 204 AATGCAATAGTATTCACCTTACATTTTCAAAATGAGACCTTGGAAAGACGACCATC 263

Db 355 AATGGATGGCCCTCTGGAATCTTCTTTCCGAACGAAGAAACACCCCGCGTATTT 414
 QY 264 ATTATGCTGAACCTGGCTGACAGATCTGCTGTATGTACCAAGCTTCCCTTCTATTT 323
 Db 415 TACATGGCCAACTGGGCTTGGCCGACCTCTCTGTCTCATCTGTGTTCCCTGAAATTC 474
 QY 324 CACTATATGCCAGTGGCCGAAACTGGATCTTGAATTTCAATGTGTATGTTATCCGC 383
 Db 475 TCCTACACCTTACATGGAACAACCTGGGTTCAGGGAGGCCCTTGACAGGTCATTT 534
 QY 384 TTACAGCTTCATTTCAACCTGTATAGCAGCATCTCTTCTCACTGTCTTCAAGCATCTTC 443
 Db 535 GGCTTTTCTATAGTAACATGTATGCTCATCTCTTCAATGACCTGCTCAAGGTGACAG 594
 QY 444 CGCTACTGTGTATCATTCACCAATGAGCTGCTTTTCCATTCAAAAATCTCGATGTGCA 503
 Db 595 AGGTACTGGGTATCGTGAACCCCATGAGGACACCCCAAGAAAGGCAACATGCGCGTT 654
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 Db 655 GGCCTCTCTTGGCAATCTGCTCTGATTTTCTGTGTACCATTC 699

Search completed: January 30, 2003, 06:48:46
 Job time : 78 secs

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Sequence 1, Application US/08476976
Patent No. 5874400
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,976
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 232..1416
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 232
US-08-476-976-1

Query Match          9.0%; Score 97.8; DB 2; Length 1475;
Best Local Similarity 52.6%; Pred. No. 4.3e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
QY 144 CTCAGATGCACTACCTCCGTTATTATGACATTATCTTCGCGGAGATTCCAGGC 203
DB 442 CTGACCAAGGCTTCTTCGCGGTCTACATTAATGTTGTGATGGTTGCCAGT 501
QY 204 AATGCAATGATGATTCACCTTTCATTTTCAAAATGAGACCTTGAAGAGACGACCATC 263
DB 502 AATGGCAATGGCCCTCTGATCTTCCTTTCCGAAAGAAAGAACACCCGCCGTGATT 561
QY 264 AATATGCTGAACCTGGCGCTGACAGATCTGCTGATCTGACACGCTCCCTTCTGATT 323
DB 562 TACTATGGCCAACTGGGCGCTTGGCGACCTCTCTCTGATCTGTTCCCTCGAAGATC 621
QY 324 CACTACTATCCAGTGGCGAAGAACTGATCTTTGGAGATTTCATGTAAGTTATCCGC 383
DB 622 TCTACACCACTACATGCGACAACTGGGTCTAAGGAGGCCCTGTGCAAGTGTCTATT 681
QY 384 TTGAGCTTCACTTTCAACCTGTATAGACAGATCCCTTCTCAGCTGTTTGAAGATCTTC 443
DB 682 GGGTTTTTCTATGTAACATGTAATGCTCATCTCTTCAATGACCTGCGCTGAGCGTGAAG 741

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QY 444 CGCTACTGTGTGATCATTCACCAATAGAGTGTCTTTTCATTCAACAACCTCATGTCGA 503
DB 742 AGGTACTGGGTATCTGTGAACCCCATGGACACCCAGAGAGGCAACATGCGCGTT 801
QY 504 GTTGTAGCCTGTGCTGTGTGTGATCATTTTCATGTAAGTGTGTC 548
DB 802 GGGTCTCCTTGGCAATCTGGCTCTGATTTTCTGTGATCCATC 846

RESULT 12
US-08-474-410-1
Sequence 1, Application US/08474410
Patent No. 6043212
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 232..1416
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 232
US-08-474-410-1

Query Match          9.0%; Score 97.8; DB 3; Length 1475;
Best Local Similarity 52.6%; Pred. No. 4.3e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
QY 144 CTCAGATGCACTACCTCCGTTATTATGACATTATCTTCGCGGAGATTTCAGGC 203
DB 442 CTGACCAAGGCTTCTTCGCGGTCTACATTAATGTTGTGATGGTTGCCAGT 501
QY 204 AATGCAATGATGATTCACCTTTCATTTTCAAAATGAGACCTTGAAGAGACGACCATC 263
DB 502 AATGGCAATGGCCCTCTGATCTTCCTTTCCGAAAGAAAGAACACCCGCCGTGATT 561
QY 264 AATATGCTGAACCTGGCGCTGACAGATCTGCTGATCTGACACGCTCCCTTCTGATT 323

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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 370:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 28..1011
US-08-513-9748-370

Query Match 9.3%; Score 100; DB 3; Length 1020;
Best Local Similarity 57.5%; Pred. No. 7,3e-21;
Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

2y 270 CTGACCTGGCTGACAGATCTGCTATCTGACAGCCCTCCCTTCCTGATTCATC 329
Db 223 CTGACCTGGCTGACAGATCTGCTATCTGACAGCCCTCCCTTCCTGATTCATC 282
2y 330 TATGCCAGTGGCCAAAATCTGATTTTGAGATTTTCATGTGAATTTATCCGCTTCA 389
Db 283 TACGCCAGAGGGGACCACTGGCCCTTCGAGACCTGGCCCTTCGATGCTTCTC 342
2y 390 TTCCATTTCACTGATATAGAGATCTCTCTCACTGCTTTTCAAGATCTCCGCTAC 449
Db 343 TTCTATGCCATCTACATGAGAGATCTCTCTCACTGATTCATTCAGAGCTAC 402
2y 450 TGTGTATCATTCACCAATAGCTGCTTTTCATTCACAAATCTCATGTGAGTT--- 506
Db 403 CTGGGATCTGCCACCCCTGGCTTCTCTGACAGAGGTGGAGGTGGCGGCTGCTGG 462
2y 507 GTAGCTGTCTGTGTGTGTGATTCATTCATCTGATGCTGTCTATTCGAGTCTTGG 566
Db 463 GTAGT 522
2y 567 ATACATCAACCAAGAGCAAGATCAAGATCAAGCTCTCTGACCTCTAC 614
Db 523 GCTGCCAGAGCATTCACGCGCACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 570

RESULT 8
US-08-097-938-1
Sequence 1, Application US/08097938
Patent No. 5629174

GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,938
FILING DATE: 26-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22803-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 232..1416
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 232
US-08-097-938-1

Query Match 9.0%; Score 97.8; DB 1; Length 1475;
Best Local Similarity 52.6%; Pred. No. 4.3e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 144 CTGAAGATGACCTACCTCCCTGTTATTTATGCAATTCCTCTGCGGATTTCCAGGC 203
Db 442 CTGACACGGTCTTCTTCGGTGTCTACATTTGTGTGTGTGTGTGTGTGTGTGTGT 501
Qy 204 AATGACAGTATGATATCATCTTCAATTTGAAATGAGACCTTGGAGAGACACCATC 263
Db 502 AATGACATGCGCTCTGATCTTCTTTCCGACGAAAGAAACACCCCGCTGATT 561
Qy 264 AATATGCTGACCTGCGCTGACAGATCTGCTATCTGACACACCTCCCTCTGATT 323
Db 562 TACATGGCAACCTGGCTTGGCGGACCTCTCTGTGATGTGTGTGTGTGTGTGTGTGTGT 621
Qy 324 CACTATATGCTGACCTGCGGAAATCTGATCTTTGGAATTTCAATGTGTGTGTGTGTGT 383
Db 622 TCTTACCACTTACATGCAACACTGGGTCTACCGGGAGGCGCTGTCAAGTCTCATTT 681
Qy 384 TTGAGCTTCAATTTCAACCTGATATGACAGATCTCTTCTCACTGTTTACATCTTC 443
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Qy 444 CGTACTGTGTGATCATTCACCAATAGAGTGTCTTTTCAATTCACAAATCTCATGTGCA 503
Db 742 AGTACTGGGT 801
Qy 504 GTTGTACCTGT 548
Db 802 GCGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 846

RESULT 9
US-08-476-000-1
Sequence 1, Application US/08476000
Patent No. 5716789

GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,000


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1 APPLICATION NUMBER: US/08/749,707
2 FILING DATE: 15-NOV-1996
3 CLASSIFICATION: 536
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Adler, Reid G.
6 REGISTRATION NUMBER: 30,988
7 REFERENCE/DOCKET NUMBER: 044481-5010-01-US
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: 202-467-7000
10 TELEFAX: 202-467-7176
11 INFORMATION FOR SEQ ID NO: 1:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 1996 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: cDNA
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: 625..1626
21 US-08-749-707-1
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23 Query Match 11.9%; Score 129; DB 3; Length 1996;
24 Best Local Similarity 50.1%; Pred. No. 1,4e-29;
25 Matches 380; Conservative 0; Mismatches 370; Indels 9; Gaps 2;
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27 QY 108 GCTGCTTTTGGAAATTCGACATGATGAAACATCCCACTCAAGATGACTACTCCCTGTT 167
28 DB 649 GCAACTTCGAAAATCTGGCTGGCAGCAGAGGCTGCCCTGAAAAGTACTTACCTTTCATT 708
29 QY 168 ATTATGCACTTATCTTCTCTGTGGGATTTCCAGGCAATGCAATGATATATCCACTTAC 227
30 DB 709 TTTATAGGATTCGATTCGTTCTGTGGGAGTCTTGGAAATACCATATGTTTTCAGGCTAC 768
31 QY 228 ATTTTCAAAATGAGACCTTGGAGAGCAGCAGCATATATGCTGCAACCTGGCCCTGCACA 287
32 DB 769 ATCTTCTCTCGAAGAACTGAAACAGCAGATATATTTATCTCTTTAACTTCTCTGTCT 828
33 QY 288 GATCTGCTGATTCGACCAAGCCTCCCTCTCTGATTCATCTATGCGAGTGGCGAAAC 347
34 DB 829 GACTTACGCTTTCTGTGACCCCTCCCATGCTGATTAAGAGATTAAGCAATGG--AAAC 885
35 QY 348 TGGATCTTGGAGATTTCAATGTGTAAGTTATCCGCTTCAAGCTTCCATTCACTGTAT 407
36 DB 886 TGGATATATGAGAGAGCTGCTCTGCAATAAGCAACCGATATGTGCTTACATGCCAACCTCTAT 945
37 QY 408 AGCAGCATCCCTCTCCACCTGTTTACAGATCTTCCGCTACTGTGATCATTTACCA 467
38 DB 946 ACGCAGCATCTCTTCTCACCTTATACAGCAATAGATGATATCTGATATATTAATATCTCT 1005
39 QY 468 ATGAGCTGCTTTTCATTTCACAAACTGATGATGAGCTGTGAGCCTGTGGTGTGG 527
40 DB 1006 TTCCGAGAAACACTTTCGCAAAAGAAAGATTGTGATTTTATCTCCTTGGCAATTTGG 1065
41 QY 528 ATCATTTCACTGTGAGCTGTGATTCCTCCATGACCTTCTTGATTCACATCAACAACAGAGCC 587
42 DB 1066 GTTTTAACTAAGCTTATGATTAATCTACCACTTACCTCCCTTATTAATATCTGTTAATCTGAC 1125
43 QY 588 AAGCAGATAGCCTGTCTTCGACCTCAACAGATCCGATGAGTGAATCAATCAATTAAGTGTAC 647
44 DB 1126 AATGGCACACCTGTATATGATTTTGGCAAGTCTGAGAGCCCAACTACAACTCACTTATAC 1185
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46 DB 1186 AGCATGTGTCTAATACAGTGTGGGGTCTTATTTCTCTCTTTTGTGATGTGTTTCTTTTAT 1245
47 QY 708 ACGACGATT-----ATTCACACTCTGACCCATGACATGCAAACTGACAGCTGCTTAAAG 761
48 DB 1246 TACAAGATTGCTCTTCTTCTTAAGCAGAGGAATAGGCGAGTGTGCTACTGCTCTGCCCCCTT 1305
49 QY 762 CAGAAAGACAGAAAGCTTACATTTCTGTACTCTTGTGATTTTATAGTATGTTTTTATACC 821
50 DB 1306 GAAAGAGCTTCAACTGTGTATCATGAGAGGTGTAAATCTTCTCTGTGCTTTTATACAGCC 1365

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M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga,
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multiplexed sequencer. *Genome Res.*
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES

source

1. 422
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 /clone="F53020.F11"
 /clone_lib="RIKEN full-length enriched, adult male kidney"
 /sex="male"
 /tissue_type="kidney"
 /dev_stage="adult"
 /lab_host="SOLR"
 /note="Site 1: XhoI; Site 2: SstI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer 15'
 GAGGAGAGAGCGCGCGACCTCTTTTCTTTTCTTTT 3'. cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence 15'
 GAGGAGAGAGAGATCGAAGCTCAATTAATTAATTAACCCCCCCC 3'.
 cDNA was cleaved with XhoI and SstI."
 BASE COUNT 104 a 100 c 88 g 130 t
 ORIGIN

Query Match 9.3%; Score 100; DB 10; Length 422;
 Best Local Similarity 57.5%; Pred. No. 1.2e-17;
 Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;
 Y 112 CTTTGAATGACCTGATGAATCAATCCACTCAAGATGACCTCCCTGTTATTT 171
 |||||
 b 75 CTTGAGAGATTGGTTGGCAACAGAGGCTATCTGAATAGTACTCTCTGCAATTT 134
 |||||
 Y 172 ATGCAATATCTTCTCGTGGGATTTTCAGGCAATGAGTATTCACCTTAATTT 231
 |||||
 b 135 ATGCAATGAGTTCAATTTTGGACTCTTGGGATGTCAGTGTGTGGCTACTCTT 194
 |||||
 Y 232 TCAAAATGAGACTTGGAGAGAGACATCATATATGCTGAACCTGGCTGCACAGATC 291
 |||||
 b 195 TCTGATGAGAACTGGAACAGACAGATGTCTATCTTTTAACTTTTCATCTGACT 254
 |||||
 Y 292 TCGTATCTGACACAGCTCCCTCTGATTCATCACTATGCGAGGAGAAACCTGGA 351
 |||||
 b 255 TTGCTTCTGTCGACCTCTCCATCTCTATTAAGATTAAGCAAT--GATAGGGGA 311
 |||||
 Y 352 TCTTGGAGATTTCATGTATTAAGTTATCGCTTCAGCTTCAATTCACCTGTATGCA 411
 |||||
 b 312 CTTATGAGATGTTCTCTGATTAAGCAACGATATGCTTCAACCAACTCTACACCA 371
 |||||
 Y 412 GCATCTCTCTCTCACTGTGTTGAGCATCTTCGCTACGTGTGATCA 459
 |||||
 b 372 GCATCTCTCTCTCACTTTCATTAGCATGAGCGATATCTGTGATCA 419
 |||||

RESULT 14
 BG924078 801 bp mRNA linear EST 05-JUN-2001
 LOCUS 60282365F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4952433 5',
 DEFINITION mRNA sequence.
 ACCESSION BG924078
 VERSION BG924078.1 GI:14304554
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCES 1 (bases 1 to 801)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL10910 row: e column: 10
 High quality sequence start: 25
 High quality sequence stop: 799.
 Location/Qualifiers
 1. 801

FEATURES

source

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4952433"
 /clone_lib="NCI CGAP Mam6"
 /sex="Female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"
 BASE COUNT 166 a 228 c 193 g 213 t
 ORIGIN

Query Match 9.2%; Score 99.6; DB 13; Length 801;
 Best Local Similarity 53.3%; Pred. No. 2e-17;
 Matches 210; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
 QY 155 CTACCTCCCTGTTATTTATGACATTAATCTTCTCGTGGGATTTCCAGGCAATGAGTAGT 214
 |||||
 Db 188 CTTTCTCCGCGTGTCACTATTTGTTGTTGATTTGTTGCCAGTATGAGCAATGC 247
 |||||
 QY 215 GATATCACTTAATTTTCAAAATGAGACCTTGAAGAGAGACCATCATTAATGCTGA 274
 |||||
 Db 248 CTTCTGATTTCTCTTTTCCGAGCAAGAAAGAAACCCCGCTGTGATTAACAGGCCAA 307
 |||||
 QY 275 CTTGGCTGCAGAGATCTGCTATCTGACCAAGCTCCCTCTGATTCATCACTATGAC 334
 |||||
 Db 308 CTTGGCTTGGCTGACCTCTCTCTGATCTGTGTTCCCTGCGCATTTGCTACACT 367
 |||||
 QY 335 CAGTGGGAAAATGGAATCTTGGAGATTCATGTGTATTAATTCCTGCTTCACTTCA 394
 |||||
 Db 368 ACAATGGCAACAATCGGCTATGAGGAGCCCTGTGCAAGTGTCTATGAGCTTTTCTA 427
 |||||
 QY 395 TTTCACCTGTATAGAGATCTCTTCTCACTGTTTATAGATCTTCCGCTACTGTGT 454
 |||||
 Db 428 TGGCAACATGTATTTGCTTCACTCTTTCATGACCTGCTCAGGCTGACAGATACCTGGT 487
 |||||
 QY 455 GATCATTCACCAATAGAGCTTTTTCATTCACAAAACTGCATGTGCACTGTAGCTG 514
 |||||

and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence 15',
GAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCCC 3'). cDNA was cleaved with BamHI and XhoI. Vector: a modified phineescript KS(+) after bulk excision from Lambda FliC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES

source

Location/Qualifiers
1..2542
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:5430432J15"
/db_xref="MGI:1897121"
/db_xref="taxon:10090"
/clone="5430432J15"
/issue_type="head"
/clone_id="Riken full-length enriched mouse cDNA library"
/dev_stage="6 days neonate"
1..2542
/gene="P2ry2"
484..1605
/gene="P2ry2"
/note="data source:MGI, source key:MGI:105107, evidence:ISS
putative receptor P2Y, G-protein coupled 2 putative"
/codon_start=1
/protein_id="BAB30719.1"
/db_xref="GI:12856589"
/db_xref="MGI:105107"
/translation="MAADLEPMNASTNGTMEGDELGYKCFNEDFKVLLPVSGYVC
VIGLCINVALYIFLCRLTMNASTTYMFLAVSDLYASLILVYVARGHWPSS
TVLCRLPFLFYNLVCSILFLCISVHRCGLRPHSRMARARARVAAYVYL
VLAQAPVLYPTTSVGRTRITCHDTSARLFSFPAVSSVMGLLPAVPSVILCY
VLMARLLPAGTGTGLPPARKSVRTTALVAVALCPPLPRLTLLYSRSLDL
SCHTIAVIMAYKITRPLASANSCLDPLVFLAGORLVRPARAKPTEPTPSPQAR
KGIHPNMTVRDLVSVDSDSRSTESTPAGSETKDIRL"

CDS

gene

BASE COUNT 517 a 737 c 705 g 582 t 1 others

NIGIN

Query Match 9.3%; Score 100.4; DB 11; Length 2542;
Best Local Similarity 51.3%; Pred. No. 2e-17;
Matches 233; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

160 TCCCTGTTATTTATGATATCTCTCGTGGGATTTCCAGGGAAGAGCTAGTATAT 219
b 590 TCCCTGTTATTTATGATATCTCTCGTGGGATTTCCAGGGAAGAGCTAGTATAT 219
220 CCACTTACATTTTCAAAATGAGACCTTGGAGAGACACCATATATATGTAACCTGG 279
b 650 ATATCTTCTTATGCGCGCTCAAAACCTGGAACCGCTCCACACCTATAGTTTACCTGG 709
280 CCGTGCAGATCTGCTGATCTGACGACGCTCCCTCTCGATTCACATCAGTACGAGT 339
b 710 CAGTTTGGAGCTCTCTGAGGAGCGGCTCGGCTGTTGTTTATTAACGCGCGGG 769
340 GCGAAAGTGAATCTTGAAGATTTATGATTAATCGCTTGAAGTTCATTCATTC 399
b 770 GTGACACATGGCCATTTAGACAGGTGCTGCAAGCTGAGCGGTTCTCTTACACCA 829
400 ACCCTGATAGCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 459
b 830 ACCCTGATAGCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 889
460 TTCACCAATGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 519
b 890 TCGGCGCTTCTGACCTCCCGCGTGGGCGCGCGCGCTTATGCGCGCGGAGTGGCGG 949
520 TGGTGTGATCATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 579
b 950 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009

cy 580 ACAGGACCAACAGATCAGCTGTCTGACCTCAC 613
db 1010 TCGCGGGAACCCGATCATCTTGCATGACACTC 1043

RESULT 12

AK005013

LOCUS

DEFINITION

AK005013 3001 bp mRNA linear HTC 19-JAN-2002
Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone:1300015C04; putative receptor P2Y, G-protein
coupled 2, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AK005013
AK005013.1 GI:12836638
HTC; CAP trapper.
Mus musculus (strain: C57BL/6J) adult male liver cDNA to mRNA,
clone:1300015C04.
Mus musculus

ORGANISM

REFERENCE

AUTHORS

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, M., Gaasterland, F., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombarts, P., Nordone, P.,
Rings, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Seaki, H.,
Sato, K., Schombach, C., Seyer, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyooka, K., Wang, K.H., Welz, C., Whitaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
JOURNAL
MEDLINE
PUBMED
11217851
5 (bases 1 to 3001)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,

BASE COUNT 83 a 163 c 125 g 108 t 12 others
 RIGIN

Query Match 9.8%; Score 106.2; DB 12; Length 491;
 Best Local Similarity 59.4%; Pred. No. 2.1e-19;
 Matches 168; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

145 TCAAGATGCACTACCTCCCTGTTATTTATTTAGCATTTATCTTCCTGCGGATTTCCAGGCA 204
 |||||
 209 TCAAGTTCATCTCCGCTGCCCATCTCCACGCAATCGCTTCGTGGTGAGTCCCTCCCA 268
 |||||
 205 ATGCACTAGTATGATTCACATTTACATTTTCAAAATGAGACCTTGGAGAGACACCATCA 264
 |||||
 269 ACTCTGGGCGCATGTGATTTTGTCTCCAGAGTAGGCGCTGGAGCGCACACCACTT 328
 |||||
 265 TTATGCTGCAACCTGGCGTGCACAGATCTGTATCTGACAGCGCTCCCTCTCGATTC 324
 |||||
 329 ACATGTTTAACTTACAGCATCTGACACGCTCTATGCTCTCCCTCCCACTGGATCT 388
 |||||
 325 ACTACTATGCGCAGTGGGAAACTGATCTTTGGAGATTTTCATGTGTAAGTTATCCGCT 384
 |||||
 389 ACTACTACCTGACCCCAACACTGCGCTCCNNNGAAGTGTGTGNNNNNNNNNGCT 448
 |||||
 385 TCAGCTTCATTTCAACCTGTATAGACGACATCTCTCCCTCCAC 427
 |||||
 449 TTTCTCTTACCGCAACTCTTACAGACGACATCTCTCTCTGAC 491
 |||||

RESULT 9
 LOCUS AL588350 609 bp mRNA linear EST 02-MAR-2001
 DEFINITION AL588350 BP Chicken Brain Library Gallus gallus cDNA clone
 ROS071B08, mRNA sequence.

ACCESSION AL588350
 VERSION AL588350.1 GI:13193384
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 609)
 MURRAY, F.
 BP Chicken Brain Library
 Unpublished (2001)
 CONTACT: Frazer Murray
 Dept. Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UK
 Tel: +44 (0)131 527 4200
 Fax: +44 (0)131 440 0434
 Email: frazer.murray@rosc.ac.uk
 GCGGCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
 (*6854-
 Seq primer: T7.

FEATURES
 source
 1. 609
 Location/Qualifiers
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /clone_lib="ROS071B08"
 /clone_1ib="BP Chicken Brain Library"
 /issue_type="Brain"
 /dev_stage="Unknown"
 /lab_host="DH10B"
 /note="Vector: pSPORT1, Site 1: NotI, Site 2: SalI; Cloned
 unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
 5' TCACCTCGAG 3' ; 3' adaptor sequence: 5'
 GCGGCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
 Clontech (*6854-1)"

BASE COUNT 101 a 199 c 189 g 117 t 3 others
 RIGIN

Query Match 9.5%; Score 103; DB 9; Length 609;
 Best Local Similarity 59.1%; Pred. No. 1.9e-18;
 Matches 175; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

145 TCAAGATGCACTACCTCCCTGTTATTTATTTAGCATTTATCTTCCTGCGGATTTCCAGGCA 204
 |||||
 293 TCAAGTTCATCTCCGCTGCCCATCTCCACGCAATCGCTTCGTGGTGAGTCCCTCCCA 352
 |||||
 205 ATGCACTAGTATGATTCACATTTTCAAAATGAGACCTTGGAGAGACACCATCA 264
 |||||
 353 ACAGCGGCGCATGTGATGTTGCTTCACATGCGCGGTGGAGGCGCATCTCGGTGT 412
 |||||
 265 TTATGCTGCAACCTGGCGTGCACAGATCTGTATCTGACAGCGCTCCCTCTCGATTC 324
 |||||
 413 ACATGTTTAACTTACAGCATCTGACACGCTCTATGCTCTCCCTCCCACTGGATCT 472
 |||||
 325 ACTACTATGCGCAGTGGGAAACTGATCTTTGGAGATTTTCATGTGTAAGTTATCCGCT 384
 |||||
 473 TCACTACTTCAACAAACGATCTGATCTTCGGGAGCGTCAATGTGACAGTGCAGAGGT 532
 |||||
 385 TCAGCTTCATTTCAACCTGTATAGACGACATCTCTCTCCCTCCACATC 440
 |||||
 533 TCATTTTCCACGTAACCTCTACGCGCAGCATCTGTTNCTCACGTGATAGAGCTC 588
 |||||

RESULT 10
 LOCUS A1663305 520 bp mRNA linear EST 10-MAY-1999
 DEFINITION uk27c10.y1 Sugano mouse kidney mKia Mus musculus cDNA clone
 IMAGE:1970226.5, similar to SW:P2YR_PAT P49651 P2Y PURINOCPTOR 1
 , mRNA sequence.

ACCESSION A1663305
 VERSION A1663305.1 GI:4766888
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 520)
 MARRA, M., HILLIER, L., KUCABA, T., MARTIN, J., BECK, C., WYLLIE, T.,
 UNDERWOOD, K., STEPTOE, M., THEISING, B., ALLEN, M., BOWERS, Y., PERSON
 B., SWALLER, T., GIBBONS, M., PAGE, D., HARVEY, N., SCHURK, R., RITTER
 E., KOHN, S., SHIN, T., JACKSON, Y., CARDENAS, M., MCCANN, R.,
 WATERSTON, R. and WILSON, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Other ESTs: uk27c10.x1

TITLE
 JOURNAL
 COMMENT
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAG Consortium (info@image.lml.gov) for further information.
 MGI:986966
 Seq primer: custom primer used
 High quality sequence stop: 490.

FEATURES
 source
 1. 520
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone_lib="IMAGE:1970226"
 /clone_1ib="Sugano mouse kidney mKia"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pME188-Flu3; Site 1: DraIII
 (CACTGATG); Site 2: DraIII (CAACATGG); 1st strand cDNA
 was primed with an oligo(dT) primer
 (ATGTGCGCTTTTCTTTTCTTTTCTTTT) ; double-stranded cDNA was
 ligated to a DraIII adaptor (TGTGGCGCTTACGCG) ; digested

```

Db 421 GCTTCCTGGGATCTGCTACCAATGAATCACTGGTTGGCGAAGGCGGAATGCTC 480
Oy 505 TTGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 564
Db 481 GGATTAATTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Oy 565 TGATCAATCAACCAACGACGACCAATGATGATGATGATGATGATGATGATGATG 624
Db 541 TTGTACACACAGTTCATGAGGAGACACACACACACACACACACACACACACAC 600
Oy 625 AACTCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 650
Db 601 TATTGACCACTMTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 626

RESULT 5
LOCUS BG402029 877 bp mRNA linear EST 12-MAR-2001
DEFINITION 60246748F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4594810 5',
ACCESSION BG402029
VERSION BG402029
KEYWORDS EST.
SOURCE BG402029.1 GI:13295477
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1336 row: P column: 11
High quality sequence stop: 542.
Location/Qualifiers
1..877
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4594810"
/clone_1ib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccgcgcgc); Site 2: SfiI (ggcgatcggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATTAATGAGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCCGACGCGGCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained insert
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH-MGC Library."

BASE COUNT 198 a 221 c 199 g 259 t
ORIGIN
Query Match 10.1%; Score 109.4; DB 12; Length 877;
Best Local Similarity 58.5%; Pred. No. 3.2e-20;
Matches 210; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Oy 108 GCTGCTTTGGAATGCACTGATGAAAACATCCCACTCAATGATGCTACTCTCTGTT 167
Db 125 GCAACTGTGCAAAACGCGCGGAGAGAGAGCGCTGCGTGAAGAAATGATCACTTTTCAATT 184
Oy 168 ATTATGCGATTATCTCTCTGCGGATTTTCAAGGCAATGATGATATCCACTTAC 227

```

```

Db 185 TTTATGAGATTGAGTTCCTGTGGAGAGCTTGGAAATACATTTGTTTACGGCTAC 244
Oy 228 ATTTCAAAATGAGACTTGAAGAGACACCATCATTAATGATGAACTGGCGCTGACA 287
Db 245 ATCTTCTCTGTAAGAACTGGAAGAGAGATATATTTATCTTTTAACTCTCTGCTCT 304
Oy 288 GATTCGCTGATATGACCAAGCTCCCTCTCTGATTACTACTATGACGAGCGGAAAAC 347
Db 305 GACTTACCTTTCGTGTGACCTCCCAATGATGATGATGATGATGATGATGATGATG 361
Oy 348 TGGATCTTGGAGATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 407
Db 362 TGGATATATGAGAGAGCTGCTGCAATGACACCATATGCTTCAATGCAACCTCTAT 421
Oy 408 AGCAGCATCTCTTCTCTGACCTGTTTACGATCTCCGCTACTGTGTGATTCATTCACC 466
Db 422 ACCAGCATCTCTTCTCTGATCTTTATGACATGATGATGATGATGATGATGATGATTC 480

RESULT 6
LOCUS BM426517 663 bp mRNA linear EST 30-JAN-2002
DEFINITION p6f2n.pk002.06 Normalized Chicken Abdominal Fat Library (p6f2n)
Gallus gallus cDNA clone p6f2n.pk002.06 5' similar to
epiP34956[P21R-CHICK P2Y PURINORECEPTOR 1 (ATP RECEPTOR) (P2Y1)
(PURINERGIC RECEPTOR) p1r[S33733 G protein-coupled receptor -
chicken emb|CA51716.1| (X73268) ATP receptor p2y1 [gallus gallus]],
mRNA sequence.
BM426517
BM426517.1 GI:18430913
EST.
ACCESSION BM426517.1 GI:18430913
VERSION BM426517.1
KEYWORDS EST.
SOURCE BM426517.1
ORGANISM chicken.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 663)
AUTHORS Cogburn, L.A., Morgan, R. and Burnside, J.
TITLE ESTs from Normalized Chicken fat cDNA library-USDA/IRAFs Animal
Genome Project
JOURNAL Unpublished (2002)
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Fax: 302-831-1335
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
1..663
/organism="Gallus gallus"
/strain="Commercial broiler, Ottawa Research Centre,
Leghorn"
/db_xref="taxon:9031"
/clone="p6f2n.pk002.06"
/lab_host="E. coli EMD10B"
/notes="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each developmental age
(across strains); Single pass sequencing from 5'-end"
/dev_stage="Embryonic (dl8,dl9); post-hatch (dl,w3,w7,w9
,w16,lyr)"
/lab_host="E. coli EMD10B"

BASE COUNT 102 a 223 c 210 g 121 t
ORIGIN
Query Match 10.1%; Score 108.8; DB 13; Length 663;
Best Local Similarity 57.5%; Pred. No. 4.2e-20;
Matches 188; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Oy 145 TCAAGATGACATACCCCTGTTATTTATGCAATTAATCTCTGCGGATTTCCAGGCA 204

```


RESULT 3			
BO396255			
LOCUS			
DEFINITION	641 bp	mRNA	linear
IMAGE:519307.y1	N1CHD	XCC	Emb6
STRAC:533884.5	'	mRNA	sequence.
ACCESSION	BO396255		
VERSION	BO396255.1	GI:21083932	
			EST 22-MAY-2002
			cdvna clone

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b 1 ATGAAATGACCACTAGACTATTATAGCAAAATGCTTCTGATTTCCCGATTATGACGCTCT 60
y 114 TTGGAAATTCACATGATGAAGAAACATCCACTCAAGATGACTACCTCCCTGTTATTAT 173
b 61 TTGGAAATTCACATGATGAAGAAACATCCACTCAAGATGACTACCTCCCTGTTATTAT 120
y 174 GGCAATTAATCTCTCTGAGGATTTCCAGGCAATGCACTAGTATGATATCCACTTACATTTTC 233
b 121 GGCAATTAATCTCTCTGAGGATTTCCAGGCAATGCACTAGTATGATATCCACTTACATTTTC 180
y 234 AAAATGAGACCTTGAGAGAGAGCAACCATATTATGCTGAACCTGGCTGACAGATCTG 293
b 181 AAAATGAGACCTTGAGAGAGAGCAACCATATTATGCTGAACCTGGCTGACAGATCTG 240
y 294 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTATAGCCAGTGGCAAAACTGATC 353
b 241 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTATAGCCAGTGGCAAAACTGATC 300
y 354 TTGAGAGATTTCACTGATGATTTATCCGCTTCAAGCTTCACTTTCACTGTTATGACAGC 413
b 301 TTGAGAGATTTCACTGATGATTTATCCGCTTCAAGCTTCACTTTCACTGTTATGACAGC 360
y 414 ATCCCTCTCCCTACCGCTTTCAGCATCTCCGCTACTGATGATCACTTCAACCAATGAGC 473
b 361 ATCCCTCTCCCTACCGCTTTCAGCATCTCCGCTACTGATGATCACTTCAACCAATGAGC 420
y 474 TGCTTTTCATTCACAAAACGATGAGTGTAGACCTGCTGCTGCTGCTGATCAT 533
b 421 TGCTTTTCATTCACAAAACGATGAGTGTAGACCTGCTGCTGCTGCTGATCAT 480
y 534 TCACGTGATGCTGTCACTTCGATGACCTTCTTGATCACTCAACCAAGACCAACAGA 593
b 481 TCACGTGATGCTGTCACTTCGATGACCTTCTTGATCACTCAACCAAGACCAACAGA 540
y 594 TCAGCTGCTGTGACCTGACCACTGAGTGAATCACTAATCTAATAGTGTCAACCTG 653
b 541 TCAGCTGCTGTGACCTGACCACTGAGTGAATCACTAATAGTGTCAACCTA 600
y 654 ATTTGACTGCAACTACTTCTGCTCCCTCTGCTGATGACACTTGTCTATACCAAG 713
b 601 ATTTGACTGCAACTACTTCTGCTCCCTCTGCTGATGACACTTGTCTATACCAAG 660
y 714 ATTATCCACACTCTGACCACTGAGTGAATGACAGCTGCTTAAAGCAAGAACAGA 773
b 661 ATTATCCACACTCTGACCACTGAGTGAATGACAGCTGCTTAAAGCAAGAACAGA 720
y 774 AGGCTAACCAATCTGCTACTCTCTGATTTAGTATGTTTTTAACCTTCAATCTTG 833
b 721 AGGCTAACCAATCTGCTACTCTCTGATTTAGTATGTTTTTAACCTTCAATCTTG 780
y 834 AGGCTAACCAATCTGCTACTCTCTGATTTAGTATGTTTTTAACCTTCAATCTTG 893
b 781 AGGCTAACCAATCTGCTACTCTCTGATTTAGTATGTTTTTAACCTTCAATCTTG 840
y 894 CATGAAGCTTACATCGTTTCTAGACCAATTAAGTCTGCTGAACACCTTGTAACTGTTA 953
b 841 CATGAAGCTTACATCGTTTCTAGACCAATTAAGTCTGCTGAACACCTTGTAACTGTTA 900
y 954 CTATATGCTGCTGCTGACGCAAACTTCAAGAGGCTGTCTGCTCAACAGTGAATGCAAA 1013
b 901 CTATATGCTGCTGCTGACGCAAACTTCAAGAGGCTGTCTGCTCAACAGTGAATGCAAA 960
y 1014 GTTAAAGGGGAGACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACCTTGA 1067
b 961 GTTAAAGGGGAGACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACCTTGA 1014

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Oy 174 GGCATTATCTTCCTGCGGAGATTTTCAGGCAATGACAGTAGTATATCACTTACATTTTC 233
 Db 121 GGCATTATCTTCCTGCGGAGATTTTCAGGCAATGACAGTAGTATATCACTTACATTTTC 180
 Oy 234 AAAATGAGACCTTGGAAGAGACAGACCATCTTATGCTGAACCTGGCTGACAGATCTG 293
 Db 181 AAAATGAGACCTTGGAAGAGACAGACCATCTTATGCTGAACCTGGCTGACAGATCTG 240
 Oy 294 CTGTATCTGACAGGCTCCCTTCCCTGATTCATCTATAGCCAGTGGCCAAAACCTGGATC 353
 Db 241 CTGTATCTGACAGGCTCCCTTCCCTGATTCATCTATAGCCAGTGGCCAAAACCTGGATC 300
 Oy 354 TTGAGAGATTCATGATGTAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGACG 413
 Db 301 TTGAGAGATTCATGATGTAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGACG 360
 Oy 414 ATCCCTCTTCCTGACCTGTTTTCAGACATCTTCCGCTACTGTGTATCATTCACCCATGAGC 473
 Db 361 ATCCCTCTTCCTGACCTGTTTTCAGACATCTTCCGCTACTGTGTATCATTCACCCATGAGC 420
 Oy 474 TGCTTTTCCATTCACAAAACCTGATGTGAGTGTGAGCTGTGCTGTGTGTGTGATCATT 533
 Db 421 TGCTTTTCCATTCACAAAACCTGATGTGAGTGTGAGCTGTGCTGTGTGTGTGATCATT 480
 Oy 534 TCACCTGTAGCTGTGATTCGAGTACCTTCTGATGATCAATCAACCAAGAACCAACAG 593
 Db 481 TCACCTGTAGCTGTGATTCGAGTACCTTCTGATGATCAATCAACCAAGAACCAACAG 540
 Oy 594 TCAGCTGTCTGACCTTCACAGCTTCAGTGAAGTCAATCTTAAAGTGTGACAACTG 653
 Db 541 TCAGCTGTCTGACCTTCACAGCTTCAGTGAAGTCAATCTTAAAGTGTGACAACTG 600
 Oy 654 ATTTTGACTGCAACTACTTCTTGTGCTCCCTGGTGTATGATGACACTTGTGTATACCAAG 713
 Db 601 ATTTTGACTGCAACTACTTCTTGTGCTCCCTGGTGTATGATGACACTTGTGTATACCAAG 660
 Oy 714 ATTATCCACACTCTGACCTGACAGTGAAGTCAACCTGACCTTAAAGCAAGAAAGCA 773
 Db 661 ATTATCCACACTCTGACCTGACAGTGAAGTCAACCTGACCTTAAAGCAAGAAAGCA 720
 Oy 774 AGGCTAACCATCTCTGCTACTCTTGTGATTTTACGTATGTTTAACTTCCATCTTTC 833
 Db 721 AGGCTAACCATCTCTGCTACTCTTGTGATTTTACGTATGTTTAACTTCCATCTTTC 780
 Oy 834 AGGCTAACCATCTCTGCTACTCTTGTGATTTTACGTATGTTTAACTTCCATCTTTC 893
 Db 781 AGGCTAACCATCTCTGCTACTCTTGTGATTTTACGTATGTTTAACTTCCATCTTTC 840
 Oy 894 CATGAAGCTTATATGCTTCTAGACATAGCTGCTGTGAACAACCTTGTATACCTGTTA 953
 Db 841 CATGAAGCTTATATGCTTCTAGACATAGCTGCTGTGAACAACCTTGTATACCTGTTA 900
 Oy 954 CTATATGTGTGTGTGTGAGACAACTTTCAGACAGGCTGTCTCAACAGTGAATGCAAA 1013
 Db 901 CTATATGTGTGTGTGTGAGACAACTTTCAGACAGGCTGTCTCAACAGTGAATGCAAA 960
 Oy 1014 GTAAAGCGGAGACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACACCTTGA 1067
 Db 961 GTAAAGCGGAGACCTTGAGCAAGCAAGAAATTAAGTAACTCAAAACACCTTGA 1014
 RESULT 14
 ID AAD34278 standard; cDNA; 1014 BP.
 XX AAD34278;
 AC AAD34278;
 XX 16-JUN-2002 (first entry)
 DE Human AXOR89 (G-protein coupled receptor) cDNA.
 XX Human AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;
 KM Infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity;

KM anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;
 KM stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;
 KM myocardial infarction; allergy; benign prostatic hypertrophy; migraine;
 KM vomiting; psychotic; neurological disorder; anxiety; manic depression;
 KM delirium; Huntington's Disease; Gilles de la Tourette's syndrome;
 KM dementia; dyskinesia; gene; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /tag= 'a'
 FT /product= "Human AXOR89 protein"
 PN GB2365012-A.
 PD 13-FEB-2002.
 PD 10-MAY-2001; 2001GB-0011437.
 PF 11-MAY-2000; 2000US-0569137.
 PR XX
 PA (SMIR) SMITHKLINE BEECHAM CORP.
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 PI Elshourbagy N, Shabon U;
 DR WPI; 2002-332558/37.
 DR P-PSDB; AAE21803.
 PT Novel AXOR89 polypeptide and polynucleotide encoding it, useful for
 PT identifying agonists and antagonists in the treatment of diseases
 PT associated with an AXOR89 imbalance, such as cancers, diabetes or
 PT asthma -
 PS Claim 2; Page 30; 37pp; English.
 XX The invention relates to an isolated AXOR89 polypeptide (G-protein
 CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
 CC and polynucleotide encoding the polypeptide, is useful for identifying
 CC agonists and antagonists (or inhibitors) that are potentially useful in
 CC treating conditions associated with an AXOR89 imbalance, such as
 CC bacterial, fungal or protozoan infections, cancers, pain, asthma,
 CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart
 CC failure, hypotension, hypertension, urinary retention, osteoporosis,
 CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
 CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
 CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's
 CC syndrome. The polynucleotide sequence may also be used for chromosome
 CC localisation or tissue expression studies. The AXOR89 is used as a
 CC vaccine or to produce fusion proteins. The present sequence is human
 CC AXOR89 cDNA.
 XX
 SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;
 Query Match 93.7%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 8.5e-287;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 54 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTGTGATTTCCCGCATTTAGCAGCTGCT 113
 Db 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTGTGATTTCCCGCATTTAGCAGCTGCT 60
 Oy 114 TTGGAATTTGACCTGATGAAAAATCCACCTCAAGATGACATACCTCCCTGTTATTTAT 173
 Db 61 TTGGAATTTGACCTGATGAAAAATCCACCTCAAGATGACATACCTCCCTGTTATTTAT 120
 Oy 174 GGCATTATCTTCCTGCGGAGATTTTCAGGCAATGACAGTAGTATATCACTTACATTTTC 233
 Db 121 GGCATTATCTTCCTGCGGAGATTTTCAGGCAATGACAGTAGTATATCACTTACATTTTC 180
 Oy 234 AAAATGAGACCTTGGAAGAGACAGACCATCTTATGCTGAACCTGGCTGACAGATCTG 293

Severe mental retardation, Huntington's disease and Tourette's syndrome.
The present sequence encodes the P2Y1-like GPCR of the invention.
Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 93.8%; Score 1014; DB 24; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.9e-287; Indels 0; Gaps 0;
Matches 1014; Conservative 0; Mismatches 0;

54 ATGAATGAGGCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTTAGAGCTGCT 113
1 ATGAATGAGGCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTTAGAGCTGCT 60
114 TTGGAAATTCAGCTAGTAAATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 173
61 TTGGAAATTCAGCTAGTAAATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
174 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAATGATATGATCACTTACATTTTC 233
121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAATGATATGATCACTTACATTTTC 180
234 AAAATGAGACCTTGGAAAGACAGACATCATTTATGCTGAACCTGGCTGCAGAGATCTG 293
181 AAAATGAGACCTTGGAAAGACAGACATCATTTATGCTGAACCTGGCTGCAGAGATCTG 240
294 CTGTATCTGACAGACCTCCCTCTGATTCATCTACTATGCGAGTGGCGAAATCTGATC 353
241 CTGTATCTGACAGACCTCCCTCTGATTCATCTACTATGCGAGTGGCGAAATCTGATC 300
354 TTGGAATTCAGTGTAGTAAATTCGCTTCAGCTTCATTTCACTGATTAAGCAGC 413
301 TTGGAATTCAGTGTAGTAAATTCGCTTCAGCTTCATTTCACTGATTAAGCAGC 360
414 ATCTCTCTCTGACCTGTTTACAGATCTTCGCTAGCTGTGATCACTTACCCATGAGC 473
361 ATCTCTCTCTGACCTGTTTACAGATCTTCGCTAGCTGTGATCACTTACCCATGAGC 420
474 TGGCTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGTGATGATCACTT 533
421 TGGCTTTCCATTCACAAACTCGATGTCAGTGTGAGCTGTGATGATCACTT 480
534 TCACCTGAGTGTGATTCGATTCGATGATTCGATTCACATCAACAGACAGCAGC 593
481 TCACCTGAGTGTGATTCGATTCGATGATTCGATTCACATCAACAGACAGCAGC 540
594 TCACCTGAGTGTGATTCGATTCGATGATTCGATTCACATCAACAGACAGCAGC 653
541 TCACCTGAGTGTGATTCGATTCGATGATTCGATTCACATCAACAGACAGCAGC 600
654 ATTTGAGTGTGATTCGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 713
601 ATTTGAGTGTGATTCGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 660
714 ATTTGAGTGTGATTCGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 773
661 ATTTGAGTGTGATTCGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 720
774 AGGCTAACCACTTCTGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 833
721 AGGCTAACCACTTCTGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 780
834 AGGCTAACCACTTCTGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 893
781 AGGCTAACCACTTCTGATTCGATTCGATTCGATTCGATTCACATCAACAGCAGC 840
894 CATGAAGCTTACATGCTTTTACAGACATTAAGCTGCTGAAACCTTTGTAACCTGTTA 953
841 CATGAAGCTTACATGCTTTTACAGACATTAAGCTGCTGAAACCTTTGTAACCTGTTA 900
954 CATGAAGCTTACATGCTTTTACAGACATTAAGCTGCTGAAACCTTTGTAACCTGTTA 1013
901 CATGAAGCTTACATGCTTTTACAGACATTAAGCTGCTGAAACCTTTGTAACCTGTTA 960

1014 GTAAGGGGGAACCTTGAGCAAGCAAGAAATAGTACTCAACACACCTTGA 1067
961 GTAAGGGGGAACCTTGAGCAAGCAAGAAATAGTACTCAACACACCTTGA 1014

RESULT 12

AAK98323
ID AAK98323 standard; cDNA; 1014 BP.

AAK98323;
30-APR-2002 (first entry)

Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.

Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
signal transduction; human protease; GPCR disorder; gene therapy;
transgenic animal; gene; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 1..1014
FT /*tag= a
FT /product= "G-protein coupled receptor"

W0200187980-A2.

22-NOV-2001.

17-MAY-2001, 2001NO-US15957.

18-MAY-2000; 2000US-205196P.

08-AUG-2000; 2000US-0634656.

(APPL-) APPLERA CORP.

Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;

WPI; 2002-075312/10.

P-PSDB; AAO14027.

Novel isolated G-protein coupled receptor peptide useful for treating
disorder characterised by absence of, in appropriate or unwanted
expression of the receptor protein, and as immunogens to raise
antibodies -

Claim 23; Fig 1; 64pp; English.

The present specifically claimed human cDNA sequence (located on
chromosome 13) encodes a purinergic-related G-protein coupled receptor
(GPCR) of the invention. GPCRs constitute a major class of proteins
responsible for signal transduction within a cell. Upon binding of a
ligand to the extracellular portion of a GPCR, a signal is transduced
resulting in a biological or physiological change within the cell. The
GPCR proteins can be divided into five families, family I contains the
purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are
characterised by their selective responsiveness towards ATP and its
analogues, some also respond to UTP. The invention comprises a human
G-protein coupled receptor protein and encoding nucleic acids. The GPCR
protein and nucleic acids of the invention are useful in the treatment of
a disease or condition mediated by a human protease. The GPCR protein of
the invention is useful for: the development/identification of
therapeutic proteins; assays designed to quantitatively determine levels
of the protein in biological fluids; identifying compounds which modulate
the activity of the GPCR, or the interaction of the GPCR and a molecule
with which it normally interacts; and treating a disorder characterised
by an absence of, or inappropriate expression of the GPCR protein. The
GPCR nucleic acids of the invention are useful in diagnostic assays to
identify changes in the GPCR nucleic acid that lead to pathology;
controlling GPCR expression; and in gene therapy to treat patients with
aberrant GPCR gene expression. The GPCR nucleic acids can also be used in
the production of transgenic animals.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX Claim 1; Page 5175-5176; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;

Query Match 99.9%; Score 1079.4; DB 23; Length 1729;

Best Local Similarity 99.9%; Pred. No. 2.3e-306; Mismatches 1; Indels 0; Gaps 0;

Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGATGAAGAGACAACCATGAATG 60
DB 241 CATATTGCCAACTGAACTCTCTGTTTCTTGGCAAGATGAAGAGACAACCATGAATG 300
QY 61 AGGCACATGACATATTAGCAAAATGCTTCTGATTTCCCGATTAATGACAGCTGTTTGGAA 120
DB 301 AGGCACATGACATATTAGCAAAATGCTTCTGATTTCCCGATTAATGACAGCTGTTTGGAA 360
QY 121 ATTGACATGATGAAGAAATCCCACTCAAGATGACACTACCTCCCTGTTATTAATGACATTA 180
DB 361 ATTGACATGATGAAGAAATCCCACTCAAGATGACACTACCTCCCTGTTATTAATGACATTA 420
QY 181 TCTTCTCTGAGGATTTCCAGCAATGAGTATGCACTTACATTTTCAAAATGA 240
DB 421 TCTTCTCTGAGGATTTCCAGCAATGAGTATGCACTTACATTTTCAAAATGA 480
QY 241 GACCTTGGAAAGAGACACATCATTAATGCTGAACCTGCGCTGACAGATCTGCTGATTC 300
DB 481 GACCTTGGAAAGAGACACATCATTAATGCTGAACCTGCGCTGACAGATCTGCTGATTC 540
QY 301 TGACCAAGCTTCCCTCTCTGATTAATGCACTATGCGAGTGGGAAAACATGATCTTGGAG 360
DB 541 TGACCAAGCTTCCCTCTCTGATTAATGCACTATGCGAGTGGGAAAACATGATCTTGGAG 600
QY 361 ATTTCATGTAAGTATTCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 420
DB 601 ATTTCATGTAAGTATTCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 660
QY 421 TCCCTACCTGTTTACGATCTTCCGCTATGCTGATGATCAATCAACCAATGAGCTGCTTTT 480
DB 661 TCCCTACCTGTTTACGATCTTCCGCTATGCTGATGATCAATCAACCAATGAGCTGCTTTT 720
QY 481 CCATTCAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 721 CCATTCAAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 541 TAGCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 781 TAGCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840

QY 601 GTCTGACCTCACCAGTTCGGATGAACTCAATACATTAAGTGTAGCAACCTGATTTTGA 660
DB 841 GTCTGACCTCACCAGTTCGGATGAACTCAATACATTAAGTGTAGCAACCTGATTTTGA 900
QY 661 CTGCAACTACTTTTGTGCTCTCCCTTGTGTAGTACACTTTGTATACCAAGATTAATCC 720
DB 901 CTGCAACTACTTTTGTGCTCTCCCTTGTGTAGTACACTTTGTATACCAAGATTAATCC 960
QY 721 ACATCTGACCCATGAGTACGAAACTGACAGCTGCTTAAGCAGAAAGCAGAGGCTTAA 780
DB 961 ACATCTGACCCATGAGTACGAAACTGACAGCTGCTTAAGCAGAAAGCAGAGGCTTAA 1020
QY 781 CCATTGCTACTCTCTGCACTTTTACATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 1021 CCATTGCTACTCTCTGCACTTTTACATGATGATGATGATGATGATGATGATGATGATG 1080
QY 841 TTGGATGCAATCTCGCTGCTTCAATCAATGATGATGATGATGATGATGATGATGATGATG 900
DB 1081 TTGGATGCAATCTCGCTGCTTCAATCAATGATGATGATGATGATGATGATGATGATGATG 1140
QY 901 CTACATGTTTCTGACATTAAGTGTGCTGCAACCTTTGTAACCTGTTACTATATG 960
DB 1141 CTACATGTTTCTGACATTAAGTGTGCTGCAACCTTTGTAACCTGTTACTATATG 1200
QY 961 TGTGTGTAGGAGCAACTTTGAGAGGCTGTCTGCTCAACAGTGTAGTCAAGTAAAG 1020
DB 1201 TGTGTGTAGGAGCAACTTTGAGAGGCTGTCTGCTCAACAGTGTAGTCAAGTAAAG 1260
QY 1021 GGAACCTTGACCAAGCAAGAAATTAATGTAATCTCAACACCTTGAATATTTTCAATTA 1080
DB 1261 GGAACCTTGACCAAGCAAGAAATTAATGTAATCTCAACACCTTGAATATTTTCAATTA 1320
QY 1081 C 1081
DB 1321 C 1321

RESULT 6
ABV29909
ID ABV29909 standard; cDNA; 1729 BP.
XX AC
XX ABV29909;
XX AC
XX 16-SEP-2002 (first entry)
XX DT
XX XX
DE Human prostate expression marker cDNA 2990.
XX DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO2001060860-A2.
XX PD
XX 23-AUG-2001.
XX PF
XX 20-FEB-2001; 2001WO-US05171.
XX PR
XX 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of

XX 30-DEC-1999; 99US-0475790.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Glucksmann MA, White D;
 PI
 XX
 XX MPI: 2001-432880/46.
 DR P-PSDB; AAU04584.
 PT Novel isolated 26904, 38911 and 39404 polypeptides which are seven
 PT transmembrane proteins belonging to superfamily of G-protein-coupled
 PT receptors, useful for treating disorders of spleen, lung, liver, brain
 PT and kidney -
 PS
 PS Claim 2, Fig 1; 164pp; English.
 CC The sequence encodes a novel human seven transmembrane domain
 CC protein belonging to the G-protein coupled receptor (GPCR) superfamily,
 CC protein 39404. The receptor is useful in drug screening assays, to
 CC identify compounds that modulate receptor activity and/or interact with
 CC the receptor, and for producing antibodies specific for the receptor, its
 CC regions or fragments. The receptor is useful for treating/diagnosing a
 CC 26904, 38911 and 39404 protein-associated disorder characterised by
 CC aberrant expression or activity of the protein, for monitoring
 CC therapeutic effect during clinical trials and other treatment, as bait
 CC proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic
 CC analysis. The proteins and nucleic acids encoding them are useful for
 CC diagnosis and treatment of disorders selected from disorders of the
 CC spleen, lung such as Good pasture's syndrome, liver such as viral
 CC hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells
 CC such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
 CC disease, colon such as Crohn's disease, uterus and endometrium such as
 CC endometriosis, T-cell disorders such as systemic lupus erythematosus,
 CC diseases of the skin such as actinic keratosis, disorders of the heart
 CC such as myocarditis, disorders involving blood vessels such as Kawasaki
 CC syndrome, disorders involving the thymus such as DiGeorge syndrome,
 CC disorders involving B-cells such as peripheral B-cell neoplasms,
 CC disorders of the breast such as inflammations, and disorders involving
 CC the testis and epididymis such as teratoma. Numerous examples of
 CC each type of disorder are given in the specification.
 XX
 XX Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;
 30
 Query Match 99.9%; Score 1079.4; DB 22; Length 1729;
 Best Local Similarity 99.9%; Pred. No. 2,3e-306;
 Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 2Y 1 CATATTGCCAACTGAACCTCTCTGTTTCTTGCAAGTGAAGAGACCAACATGAATG 60
 2Y 241 CATATTGCCAACTGAACCTCTCTGTTTCTTGCAAGTGAAGAGACCAACATGAATG 300
 2Y 61 AGGCACCTAGACTATTAGCAAAATGCTCTGATTTCCCGATTTAGCACTGCTTTGGAA 120
 2Y 301 AGGCACCTAGACTATTAGCAAAATGCTCTGATTTCCCGATTTAGCACTGCTTTGGAA 360
 2Y 121 ATTGCACTGATGAAGAACATCCCACTCAAGATGACCTACCTGCTGTTATTTATGACATTA 180
 2Y 361 ATTGCACTGATGAAGAACATCCCACTCAAGATGACCTACCTGCTGTTATTTATGACATTA 420
 2Y 181 TCTTCTCTGCGGATTTTCAGGCAATGACATGATGATATTCACATTTTCAAAATGA 240
 2Y 421 TCTTCTCTGCGGATTTTCAGGCAATGACATGATGATATTCACATTTTCAAAATGA 480
 2Y 241 GACCTTGAAGAGAGACACATCTTATGCTGAACCTGCGCTGACAGATGCTGATATC 300
 2Y 481 GACCTTGAAGAGAGACACATCTTATGCTGAACCTGCGCTGACAGATGCTGATATC 540
 2Y 301 TGACCAAGCTCTCCCTTCTGATTCATCTACTATGCAAGTGGAGAAACATGATCTTTGGAG 360
 2Y 541 TGACCAAGCTCTCCCTTCTGATTCATCTACTATGCAAGTGGAGAAACATGATCTTTGGAG 600
 2Y 361 ATTTCATGTGTAAATTTATCGCTTTCAGCTTCATTTCAACCTGTATGACATCTCTCT 420

DB 601 ATTTCATGTGTAAATTTATCGCTTTCAGCTTCATTTCAACCTGTATGACATCTCTCT 660
 QY 421 TCTTCACTGTTTTCAGCATCTTCCGCTACTGTGTGATCATTTCAACCAATGACCTGTTT 480
 DB 661 TCTTCACTGTTTTCAGCATCTTCCGCTACTGTGTGATCATTTCAACCAATGACCTGTTT 720
 QY 481 CCATTCACAAAACCTGATGTGACATGTTAGCTGTGTGTGTGTGATCATTTCACTG 540
 DB 721 CCATTCACAAAACCTGATGTGACATGTTAGCTGTGTGTGTGTGATCATTTCACTG 780
 QY 541 TAGCTGTATTCGAGTGAACCTTCTGATCAATCAACCAAGACCAACATGACCT 600
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 DB 841 GTCTGACCTGACCAAGTGTGATGAACTCAATATCTATTAAGTGTATCAACCTGATTTTGA 900
 QY 661 CTGCAACTACTTCTGCTCTCCCTTGTGTATGACACTTTGCTATACAGATTTATCC 720
 DB 901 CTGCAACTACTTCTGCTCTCCCTTGTGTATGACACTTTGCTATACAGATTTATCC 960
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 DB 1201 TGGTGTGAGGACCAACTTTCAGCAGGCTGTCTGCTCAACAGTGAAGTGAAGTGAAG 1260
 QY 1021 GGAACCTTGAAGCAAGCAAAATTAATGATCTCAACCAACCTTGAATATTTCAATTA 1080
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 QY 1081 C 1081
 DB 1321 C 1321
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 ID ABV24026 standard; cDNA; 1729 BP.
 XX AC ABV24026;
 XX 16-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 24017.
 XX
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX

XX MPI; 2002-353329/39.
 DR P-PSDB; ABB79438.
 XX
 PT New human P2Y₁₁ gene, useful for treatment and diagnosis of associated
 PT diseases, and related proteins, antibodies and modulators, encodes G
 PT protein-coupled receptor
 XX
 PS Claim 1, Page 4-5; 5pp; German.
 XX
 CC The invention relates to the human P2Y₁₁ gene (I), including its 5' and
 CC 3' untranslated regions, located on chromosome 13 and encoding a G
 CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies
 CC etc., are used for diagnosis and (gene) therapy of diseases that are
 CC (in)directly associated with (I) or its expression products. No diseases
 CC are specified but as (I) is expressed only in thyroid tissue, (I) is
 CC presumed to be involved in regulation of thyroid function. The present
 CC sequence is that of the P2Y₁₁ encoding genomic sequence.
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 SQ Sequence 5435 BP; 1509 A; 1168 C; 996 G; 1762 T; 0 other;

Query Match 100.0%; Score 1081; DB 24; Length 5435;
 Best Local Similarity 100.0%; Pred. No. 1.4e-306;
 Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 4215 C 4215

RESULT 2
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 ID AAK98324 standard; DNA; 9905 BP.

AAK98324;
 30-APR-2002 (first entry)

Human purinergic G-protein coupled receptor (GPCR) genomic DNA.
 Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
 signal transduction; human protease; GPCR disorder; gene therapy;
 transgenic animal; gene; de.

Homo sapiens.

Key Location/Qualifiers
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 replace (7338, G)
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WO2001.87980-A2.

22-NOV-2001.

17-MAY-2001; 2001WO-US15957.

18-MAY-2000; 2000US-205196P.
 08-AUG-2000; 2000US-0634656.

(APPL-) APPLERA CORP.

Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;
 MPI; 2002-075312/10.

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901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
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RESULT 14
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LOCUS DEFINITION
AX464561 Sequence 1 from Patent EP1219638.
VERSION AX464561.1 GI:21899357
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Fiddock, M.D.
AUTHORS G-protein coupled receptors having homology to the p2y
TITLE purinoreceptor 1 (p2y1)
JOURNAL Patent: EP 1219638-A 1 03-JUL-2002;

FEATURES Pfizer Limited (GB) ; Pfizer Inc. (US)
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Best Local Similarity 99.9%; Pred. No. 6,9e-253;
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Db 961 GTAAGCGGGAACCTTGAGCAAGCAAAATAATTAGTACTCAACACACCTTGA 1014
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DEFINITION Homo sapiens GPCR gene for putative G-protein coupled receptor,
AB083598
ACCESSION AB083598
VERSION AB083598.1 GI:20152259
KEYWORDS
SOURCE Homo sapiens DNA, clone:hGPCR16.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.
Identification of G protein-coupled receptor genes from the human
genome sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1014)
AUTHORS Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.
TITLE Direct Submission
JOURNAL Submitted (10-APR-2002) Shigeaki Takeda, Gunma University,
Department of Biological and Chemical, Engineering, Faculty of
Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan
(E-mail:stakeda@ce.gunma-u.ac.jp, Tel:+81-277-30-1434,
Fax:+81-277-30-1434)
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NMP"
BASE COUNT 258 a 263 c 189 g 304 t
ORIGIN
Query Match 93.8%; Score 1014; DB 9; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.7e-253;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 ATGATGAGCCACTAGACTATTAGCAATGCTTGATTTCCCGATATGACGTGCT 113
Db 1 ATGATGAGCCACTAGACTATTAGCAATGCTTGATTTCCCGATATGACGTGCT 60
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DEFINITION Homo sapiens G protein-coupled receptor (GPR80) gene, complete cds.
ACCESSION AF411109
VERSION AF411109.1 GI:16566322
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Lee, D. K., Nguyen, T., Lynch, K. R., Cheng, R., Vantli, W. B., Arkhitekt, O.,
Lewis, T., Evans, J. F., George, S. R. and O'Dowd, B. F.
Discovery and mapping of ten novel G protein-coupled receptor genes
JOURNAL Gene 275 (1), 83-91 (2001)
MEDLINE 21458557
PUBMED 11574155
REFERENCE 2 (bases 1 to 1014)
AUTHORS Lee, D. K., Nguyen, T., Lynch, K. R., Cheng, R., Vantli, W. B., Arkhitekt, O.,

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 DEFINITION Sequence 27 from Patent WO0136471.
 ACCESSION AX148186
 VERSION AX148186.1 GI:14347086
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 ORGANISM Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1014)
 CHEN, R., DANG, H.T. and LOWITZ, K.P.
 Endogenous and non-endogenous versions of human g protein-coupled
 receptors
 JOURNAL Patent: WO 0136471-A 27 25-MAY-2001;
 ARENA Pharmaceuticals, Inc. (US)
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 Best Local Similarity 100.0%; Pred. No. 2,7e-253;
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 QY 474 TGCTTTTCATTCACAAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
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 QY 1014 GTAAAGCGGAACTTGGAG 1067
 DB 961 GTAAAGCGGAACTTGGAG 1014
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 LOCUS AX379468 1014 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 1 from Patent WO0187980.
 ACCESSION AX379468
 VERSION AX379468.1 GI:19575226
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 WEI, M.H., ZHAO, Q.C., CRAVCHIK, A.C., DI FRANCESCO, V.C. and
 BEASLEY, B.M.
 TITLE Isolated human g-protein coupled receptors, nucleic acid molecules
 encoding human spect proteins, and uses thereof
 JOURNAL Patent: WO 0187980-A 1 22-NOV-2001;
 Applera Corporation Robert A. Millman Assistant Secretary (US)
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 /db_xref="taxon:9606"
 BASE COUNT 258 a 263 c 189 g 304 t
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 Best Local Similarity 100.0%; Pred. No. 2,7e-253;
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 ATGATGAGCCACTAGACTATTATAGCAAAATGCTTCTGATTTCCCGATTATGACGTGCT 60
 QY 114 TTGGAAATTCGACATGATGAAGAACATCCACATGAGATGACATCTCCCTGATTTAT 173
 DB 61 TTGGAAATTCGACATGATGAAGAACATCCACATGAGATGACATCTCCCTGATTTAT 120
 QY 174 GGCATTATCTCTCTGCGGATTTCCAGGCAATGAGATGATATTCATTAATTTTC 233
 DB 121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGAGATGATATTCATTAATTTTC 180
 QY 234 AAAATGAGACCTTGGAGAGAGACACATCATTTATGCTGAACCTGGCTGCAAGATCTG 293
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Db 140435 TGACGAGCCTCCCTCCCTGATGCTACTATGCGAGTGCGGAAACTGATCTTTGAG 140494
OY 361 ATTCATGATGTAAGTTATCCGCTCAGCTTCATTTCAACCGTATAGAGATCTCT 420
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Db 140735 GTCTGACCTTCACAGTTGCGATGAACTCAATATCTATTAAGTGGTCAACCTGATTTTGA 140794
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Db 140915 CCATCTGCTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 140974
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Db 140975 TTCGATGCAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141034
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Db 141035 CTTAATGCTTTCTGAGCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141094
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OY 1081 C 1081
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RESULT 6
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LOCUS Sequence 2 from Patent WO0149847.
DEFINITION AX191332
ACCESSION AX191332
VERSION AX191332.1 GI:15209582
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1729)
Glucksmann, M.A. and White, D.
26904, 38911, and 39404, seven-transmembrane proteins / g-protein
coupled receptors
Patent: WO 0149847-A 2 12-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
JOURNAL

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FEATURES
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location/Qualifiers
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SLVAVIPMTFLITSNTRRSACLDLTSDELNTKYNLLIATTPCLPIVYLCY
TLIIHTLHGLTOSCLKOKARPLIILLPLVYVFLPHILRIVRISRILSICSI
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NMP"
BASE COUNT 461 a 403 c 302 g 563 t
ORIGIN
Query Match 99.9%; Score 1079.4; DB 6; Length 1729;
Best Local Similarity 99.9%; Pred. No. 2.4e-270;
Matches 1080; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 241 CATATTGCCAACTGACCTCTCTGTTTCTTCAAGATGAAGAGACAACATGATG 300
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Db 481 GACCTTGAAGAGACGACATCAATATGCTGAACCTGCGCTGACAGATCTGCTGATC 300
OY 301 TGACGAGCTCCCTCTCTGATTCATCTATGCGAGTGGCGAAACTGATCTTTGAG 360
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OY 361 ATTTGATGTAAGTTATCCGCTTCAAGCTTCAATTTGAAACCTGATATACAGATCCTCT 420
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OY 721 ACACCTGACCACTGATGTCAGTCGACAGCTGCTTAAAGCAAGACGAGGCTTAA 780

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Db      8736  CCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 8795
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Db      8796  TAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8855
Qy      601  GTCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
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Db      9216  TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9275
Qy      1021  GGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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Db      9336  C 9336

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RESULT 4
AL356486/c 67645 bp DNA linear PRI 28-SEP-2001
LOCUS Human DNA sequence from clone Rpl1-721F14 on chromosome 13,
DEFINITION complete sequence.
ACCESSION AL356486
VERSION AL356486.12 GI:15808158
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 67645)
Stuice, C.
Direct Submission
Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

COMMENT

request: clonerequest@sanger.ac.uk
On Sep 28, 2001 this sequence version replaced gi:15787734.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TREMBL; Mp: MOPREP; Information on the MOPREP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormep
This sequence was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
Rpl1-721F14 is from the library RPl1-11.3 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
Rpl1-721F14 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone Rpl1-19817 is at 65646 in this
sequence. The true right end of clone Rpl1-65L19 is at 2000 in this
sequence.

FEATURES

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Matches 1081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      5024  ATTGACATGATGATAAATCCACATGAGATGACCTACTCCCTGTTATTATG 4965
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JOURNAL highly in kidney
Patent: WO 0246414-A 1.13-JUN-2002;
Bristol-Myers Squibb Company (US)

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Best Local Similarity 100.0%; Pred. No. 9.3e-271;
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1081 C 1081
1081 C 1081

RESULT 2
AB065877 1414 bp DNA linear pri 23-JUL-2002
LOCUS
DEFINITION
Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM_440.
AB065877
AB065877.1 GI:21929018
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (isolate:CBRC7TM_440) DNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Suwa,M., Sato,T., Okouchi,I., Arima,M., Futami,K., Matsumoto,S.,
Tsutsuni,S., Aburatani,H., Asai,K. and Akiyama,Y.
TITLE
Genome-wide discovery and analysis of human seven transmembrane
helix receptor genes
JOURNAL
REFERENCE
Unpublished
2 (bases 1 to 1414)
AUTHORS
Suwa,M.
DIRECT SUBMISSION
SUBMITTED (11-JUN-2001) Makiko Suwa, Computational Biology Research
Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
(E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
Tel:81-3-3599-8080, Fax:81-3-3599-8081)
COMMENT
This sequence is a seven transmembrane helix receptor candidate
predicted from the whole human genome sequences using our automated
system that contains programs of gene
finding (GeneDecoder), sequence search, motif-domain assignment and
transmembrane helix prediction.
And the sequence is submitted by the collaborative project between
[Computational Biology Research Center (CBRC), National Institute
of Advanced Industrial Science and Technology (AIST)] and [Genome
Science Division, Research Center for Advanced Science and
Technology (RCAS), University of Tokyo].
FEATURES
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